

091718819

GenCore version 5.1.6  
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:36 ; Search time 20.3333 Seconds  
(without alignments)  
33.107 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapcp 10.0 , Gapext 0.5

Searched: 283308 seqs, 36166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	100.0	54	2 JT0521	Ig kappa chain V-I
2	32	100.0	71	2 S21526	Ig kappa chain V-I
3	32	100.0	77	2 D30502	Ig kappa chain V-I
4	32	100.0	77	2 S70443	Ig kappa chain V-I
5	32	100.0	76	2 S34102	Ig kappa chain V-I
6	32	100.0	79	2 S24215	Ig kappa chain V-I
7	32	100.0	81	2 PH1048	Ig kappa chain V-I
8	32	100.0	83	2 S78489	Ig kappa chain V-I
9	32	100.0	84	2 S34059	Ig kappa chain V-I
10	32	100.0	86	2 S16826	Ig kappa chain V-I
11	32	100.0	86	2 S16834	Ig kappa chain V-I
12	32	100.0	96	2 S16836	Ig kappa chain V-I
13	32	100.0	86	2 S34086	Ig kappa chain V-I
14	32	100.0	86	2 S16840	Ig kappa chain V-I
15	32	100.0	86	2 S16837	Ig kappa chain V-I
16	32	100.0	86	2 S16833	Ig kappa chain V-I
17	32	100.0	85	2 S16830	Ig kappa chain V-I
18	32	100.0	86	2 S16824	Ig kappa chain V-I
19	32	100.0	86	2 S16820	Ig kappa chain V-I
20	32	100.0	87	2 S34098	Ig kappa chain V-I
21	32	100.0	87	2 S21523	Ig kappa chain V-I
22	32	100.0	87	2 S34097	Ig kappa chain V-I
23	32	100.0	87	2 S34084	Ig kappa chain V-I
24	32	100.0	87	2 S34083	Ig kappa chain V-I
25	32	100.0	88	2 S21528	Ig kappa chain V-I
26	32	100.0	88	2 S21525	Ig kappa chain V-I
27	32	100.0	88	2 S21520	Ig kappa chain V-I
28	32	100.0	88	2 S21522	Ig kappa chain V-I
29	32	100.0	89	2 S34104	Ig kappa chain V-I

30	32	100.0	91	2 PH1071	Ig light chain V-I
31	32	100.0	91	2 S37525	Ig kappa chain V-I
32	32	100.0	91	2 S37527	Ig kappa chain V-I
33	32	100.0	91	2 S37521	Ig kappa chain V-I
34	32	100.0	91	2 S37511	Ig kappa chain V-I
35	32	100.0	91	2 S37515	Ig kappa chain V-I
36	32	100.0	92	2 S37533	Ig kappa chain V-I
37	32	100.0	92	2 S37530	Ig kappa chain V-I
38	32	100.0	92	2 S37529	Ig kappa chain V-I
39	32	100.0	92	2 S37523	Ig kappa chain V-I
40	32	100.0	92	2 S37535	Ig kappa chain V-I
41	32	100.0	92	2 S37509	Ig kappa chain V-I
42	32	100.0	92	2 S37512	Ig kappa chain V-I
43	32	100.0	92	2 S37531	Ig kappa chain V-I
44	32	100.0	92	2 S37534	Ig kappa chain V-I
45	32	100.0	92	2 S37532	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

JT0521

Ig kappa chain V-II: region (CPI) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 00-May-1997

C:Accession: JT0521

R:Anker, R.; Conley, M.E.; Pollok, B.A.

J. Exp. Med. 169, 2109-2119, 1989

A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia

A:Reference number: JT0511; MUID:89279157; PMID:2786547

A:Accession: JT0521

A:Molecule type: mRNA

A:Residues: 1-54 <ANK>

A:Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-49/Domain: V region <VRE>

F:50-54/Domain: J region <JRE>

Query Match 100.0%; Score 32; DB 2; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 23 FTLTSS 29

RESULT 2

S21526

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence\_revision 25-Oct-1996 #text\_change 23-Jul-1999

C:Accession: S34082; S21526

R:Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34082

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <WA2>

A:Cross-references: EMBL:X66042; NID:g33318; PIDN:CAA46841.1; PID:g33319

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 71;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 23 FTLTSS 29

```
Db          64 FTLTSS 70

RESULT 3
D30502
Ig kappa chain V region (D44) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Nov-1988 #sequence_revision 33-Aug-1992 #text_change 23-Jul-1999
C:Accession: D30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: D30502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-77 <EIL>
A:Cross-references: GB:M21908; NID:g197073; PID:AAA39908.1; PID:g197074
A:Note: the authors translated the codon CAG for residue 48 as Pro
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 32; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      |||||
Db      40 FTLTSS 46

RESULT 4
S70443
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S70443
R:Cuisinier, A.X.; Fumoux, F.; Fongereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda BSV human B cell clone: an early step of differentiation of B
A:Reference number: S70442; MUID:93024508; PMID:1393695
A:Accession: S70443
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-77 <CUI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match          100.0%; Score 32; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      |||||
Db      40 FTLTSS 46

RESULT 5
S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34102
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 32; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      |||||
Db      56 FTLTSS 62

RESULT 6
S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular exc
A:Reference number: S24214; MUID:91217618; PMID:1902503
A:Accession: S24215
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:g53718; PID:CAA41178.1; PID:g930195
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 32; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      |||||
Db      44 FTLTSS 50

RESULT 7
PH0048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH0048
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.M.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective f
A:Reference number: PH0371; MUID:92381444; PMID:1512540
A:Accession: PH0048
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match          100.0%; Score 32; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      |||||
Db      56 FTLTSS 62

RESULT 8
S78489
Ig kappa chain V region (patient 28) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: S78489; S34100
R:Wagner, S.
Submitted to the EMBL Data Library, July 1992
A:Reference number: S78488
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A;Accession: S78489
A;Molecule type: DNA
A;Residues: 1-83 <WAG>
A;Cross-references: EMBL:X67184
A;Experimental source: patient 28
R;Wagner, S.D.; Iuzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34100
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-68, 'Q', 70-73, 'A', 75-83 <WAG>
A;Cross-references: EMBL:X67184
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||
Db 61 FTLTISS 67

RESULT 9
S34099
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34099
R;Wagner, S.D.; Iuzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34099
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <WAG>
A;Cross-references: EMBL:X67183
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-79/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||
Db 60 FTLTISS 66

RESULT 10
S16826
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16826; S34101
R;Blaison, G.; Kuntz, J.L.; Pasquail, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16826
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54824; NID:G33653; PIDN:CAA38593.1; PID:G33654
R;Wagner, S.D.; Iuzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34101
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAG>
A;Cross-references: EMBL:X67185
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||
Db 62 FTLTISS 68

RESULT 11
S16834
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
R;Blaison, G.; Kuntz, J.L.; Pasquail, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54832
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||
Db 62 FTLTISS 68

RESULT 12
S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
R;Blaison, G.; Kuntz, J.L.; Pasquail, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54834
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||
Db 62 FTLTISS 68
```

## RESULT 13

S34086  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34086  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed  
A:Reference number: S34076; MUID:93170387; PMID:8436174  
A:Accession: S34086  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-86 <WAG>  
A:Cross-references: EMBL:X67169  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7

Db 64 FTLTSS 70

## RESULT 14

S16840  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S16840  
R:Blaiss, G.; Kuntz, J.L.; Pasquali, J.L.  
Eur. J. Immunol. 21, 1221-1227, 1991  
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac  
A:Reference number: S16823; MUID:91243737; PMID:1903706  
A:Accession: S16840  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-86 <BLA>  
A:Cross-references: EMBL:X54838  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7

Db 62 FTLTSS 68

## RESULT 15

S16837  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S16837  
R:Blaiss, G.; Kuntz, J.L.; Pasquali, J.L.  
Eur. J. Immunol. 21, 1221-1227, 1991  
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac  
A:Reference number: S16823; MUID:91243737; PMID:1903706  
A:Accession: S16837  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-86 <BLA>  
A:Cross-references: EMBL:X54835



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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:51 ; Search time 10.6667 Seconds  
(without alignments)  
30.862 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	107	1 KV1D_HUMAN	P01596 homo sapien
2	32	100.0	108	1 KV1F_HUMAN	P01598 homo sapien
3	32	100.0	108	1 KV1G_HUMAN	P01599 homo sapien
4	32	100.0	108	1 KV1H_HUMAN	P01600 homo sapien
5	32	100.0	108	1 KV1S_HUMAN	P01611 homo sapien
6	32	100.0	108	1 KV5Q_MOUSE	P01650 mus musculu
7	32	100.0	108	1 KV5R_MOUSE	P01651 mus musculu
8	32	100.0	108	1 KV5S_MOUSE	P01652 mus musculu
9	32	100.0	108	1 KV5T_MOUSE	P01653 mus musculu
10	32	100.0	109	1 KV1T_HUMAN	P01612 homo sapien
11	32	100.0	109	1 KV3F_HUMAN	P01624 homo sapien
12	32	100.0	114	1 KV1A_MOUSE	P01632 mus musculu
13	32	100.0	114	1 KV4A_HUMAN	P01625 homo sapien
14	32	100.0	115	1 KV3I_HUMAN	P04433 homo sapien
15	32	100.0	116	1 KV3J_HUMAN	P04434 homo sapien
16	32	100.0	117	1 KV1I_HUMAN	P01601 homo sapien
17	32	100.0	117	1 KV1J_HUMAN	P01602 homo sapien
18	32	100.0	121	1 KV40_HUMAN	P06312 homo sapien
19	32	100.0	129	1 KV1W_HUMAN	P04431 homo sapien
20	32	100.0	129	1 KV1X_HUMAN	P04432 homo sapien
21	32	100.0	133	1 KV4B_HUMAN	P06313 homo sapien
22	32	100.0	134	1 KV4C_HUMAN	P06314 homo sapien
23	32	100.0	136	1 KV5B_MOUSE	P01634 mus musculu
24	30	93.8	354	1 OPST_ASTFA	P01474 astyanax fa
25	29	90.6	108	1 KV1L_HUMAN	P01604 homo sapien
26	29	90.6	108	1 KV1Q_HUMAN	P01609 homo sapien
27	29	90.6	108	1 KV1R_HUMAN	P01610 homo sapien
28	29	90.6	400	1 CN37_BOVIN	P06623 bos taurus
29	29	90.6	421	1 CN37_HUMAN	P09543 homo sapien
30	28	87.5	92	1 KV09_RABIT	P01690 oryctolagus
31	28	87.5	100	1 KV3C_HUMAN	P01621 homo sapien
32	28	87.5	104	1 KV17_RABIT	P01698 oryctolagus
33	28	87.5	107	1 KV04_RABIT	P01685 oryctolagus

34	28	87.5	108	1 KV05_RABIT	P01686 oryctolagus
35	28	87.5	108	1 KV06_RABIT	P01687 oryctolagus
36	28	87.5	108	1 KV07_RABIT	P01688 oryctolagus
37	28	87.5	108	1 KV08_RABIT	P01689 oryctolagus
38	28	87.5	108	1 KV1B_HUMAN	P01594 homo sapien
39	28	87.5	108	1 KV1E_HUMAN	P01597 homo sapien
40	28	87.5	108	1 KV1K_HUMAN	P01603 homo sapien
41	28	87.5	108	1 KV1M_HUMAN	P01605 homo sapien
42	28	87.5	108	1 KV1N_HUMAN	P01606 homo sapien
43	28	87.5	108	1 KV1P_HUMAN	P01608 homo sapien
44	28	87.5	108	1 KV1Y_HUMAN	P01612 homo sapien
45	28	87.5	108	1 KV3A_HUMAN	P01613 homo sapien

ALIGNMENTS

RESULT 1  
KV1D\_HUMAN  
ID KV1D\_HUMAN STANDARD; PRT; 107 AA.  
AC P01596;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75075135; PubMed=4216454;  
RA Milstein C.P., Deverson E.V.;  
RT "Primary structure of kappa light chain from a human myeloma protein."  
RL Eur. J. Biochem. 49:377-391(1974).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01864; K1HJAR.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region, Glycoprotein.  
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;  
Query Match 100.0%; Score 32; DB 1; Length 107;  
Best Local Similarity 100.0%; P-Ed. No. 0.92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
DB 71 FTLTSS 77

RESULT 2  
KV1F\_HUMAN  
ID KV1F\_HUMAN STANDARD; PRT; 108 AA.  
AC P01598;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region EU.  
CS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064023; PubMed=5439770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 acid sequence of the light chain."  
 RL Biochemistry 9:3155-3161(1970).  
 CC [2]  
 CC DISULFIDE BOND.  
 CC MEDLINE=71064027; PubMed=4923144;  
 CC Gal. W.E., Edelman G.M.;  
 CC "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds."  
 RL Biochemistry 9:3188-3196(1970).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC PIR; A90562; KIHJEU.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD234F2F4D88823 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.93;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
 DB 71 FTLTSS 77

## RESULT 3

KVIG\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01599;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Gal.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 kappa-type, subgroup I."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

CC MACROGLOBULIN.  
 DR PIR; A01867; KIHUGL.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.93;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
 DB 71 FTLTSS 77

## RESULT 4

KVIH\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4397974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 subgroups."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01868; KIHUGU.  
 DR HSSP; P00362; IWL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97

```
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 98 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA; 11671 MW; C8D3A61A6F8DC618 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7
Db |||||
7: FTLTISS 77

RESULT 5
KV1S_HUMAN
HID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC PC1611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
high-pressure liquid chromatography. The primary structure of a
monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
Wes).";
RL Hoppe-Sevier's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
PIR; A01877; KIHJWS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7
Db |||||
71 FTLTISS 77

RESULT 6
KV5Q_MOUSE
HID KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01650;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
PIR; B92808; KVMS09.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region UPC 61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
PIR; A92808; KVMS61.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7
Db |||||
71 FTLTISS 77

RESULT 7
KV5R_MOUSE
HID KV5R_MOUSE STANDARD; PRT; 108 AA.
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
PIR; B92808; KVMS09.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
```

KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11876 MW; 35C116BD60F79310 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
Db 71 FTLTISS 77

RESULT 8  
KV5S MOUSE STANDARD; PRT; 108 AA.  
AC P01652;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V region J606.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).  
DR PIR; A92811; KVM586.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
Db 71 FTLTISS 77

RESULT 9  
KV5T MOUSE STANDARD; PRT; 108 AA.  
AC P01653;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region W3082.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).  
DR PIR; B92811; KVM582.  
DR HSSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
Db 71 FTLTISS 77

RESULT 10  
KV5T HUMAN STANDARD; PRT; 109 AA.  
AC P01612;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-I region Mev.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83081018; PubMed=6816713;  
RA Eulitz M., Linke R.P.;  
RT "Primary structure of the variable part of an amyloidogenic Bence-Jones Protein (Mev). An unusual insertion in the third hypervariable region of a human kappa-immunoglobulin light chain.";  
RL Hoppe-Seyley's Z. Physiol. Chem. 363:1347-1358(1982).  
CC -!- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01879; KIHUMV.  
DR HSSP; P80362; IWTL.

KW KV5T MOUSE STANDARD; PRT; 108 AA.  
AC P01653;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region W3082.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).  
DR PIR; B92811; KVM582.  
DR HSSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
Db 71 FTLTISS 77

RESULT 10  
KV5T HUMAN STANDARD; PRT; 109 AA.  
AC P01612;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-I region Mev.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83081018; PubMed=6816713;  
RA Eulitz M., Linke R.P.;  
RT "Primary structure of the variable part of an amyloidogenic Bence-Jones Protein (Mev). An unusual insertion in the third hypervariable region of a human kappa-immunoglobulin light chain.";  
RL Hoppe-Seyley's Z. Physiol. Chem. 363:1347-1358(1982).  
CC -!- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01879; KIHUMV.  
DR HSSP; P80362; IWTL.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 98  
FT DOMAIN 99 108  
FT DOMAIN 109 129  
FT DISULFID 23 88  
FT NON TER 109 129  
SQ SEQUENCE 109 AA; 11870 MW; 36ABF4515D55F5A0 CRC64;  
  
Query Match 100.0%; Score 32; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
2Y : FTLTISS 7  
Db : FTLTISS 77  
  
RESULT 11  
KV3F\_HUMAN STANDARD; PRT; 109 AA.  
AC P01624;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig kappa chain V-III region POM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
BY SIMILARITY.  
SEQUENCE.  
MEDLINE=76276460; PubMed=60893;  
Klapper D.G., Capra J.D.;  
"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IGM anti-gamma globulins.";  
Ann. Immunol. (Paris) 127C:261-271 (1976).  
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.  
PIR; A01897; K3HUPM.  
HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DISULFID 23 89  
FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11922 MW; 6282:DDC6A8ABA86 CRC64;  
  
Query Match 100.0%; Score 32; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 1 FTLTISS 7  
Db : FTLTISS 77

Db 72 FTLTISS 78  
  
RESULT 12  
KV1A\_MOUSE STANDARD; PRT; 114 AA.  
ID KV1A\_MOUSE  
AC P01632;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Slc7A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81241357; PubMed=6788890;  
RA Kwan S.-P., Rudikoff S., Seidman C.G., Leder P., Scharff M.D.;  
R: "Nucleic acid and protein sequences of phosphocholine-binding light chains."  
RL J. Exp. Med. 153:1366-1370 (1981).  
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CC  
DR EMBL; U29423; AAC00033.1; -  
DR PIR; A01915; KWS7A.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 40  
FT DOMAIN 41 55  
FT DOMAIN 56 62  
FT DOMAIN 63 94  
FT DOMAIN 95 103  
FT DOMAIN 104 113  
FT DISULFID 23 94  
FT NON TER 114 114  
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;  
  
Query Match 100.0%; Score 32; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.99;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLTISS 7  
Db : FTLTISS 83  
  
RESULT 13  
KV4A\_HUMAN STANDARD; PRT; 114 AA.  
ID KV4A\_HUMAN  
AC P01625;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-IV region Len.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

```

[1]
RN SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonal immunoglobulin-L-chain of
RL subgroup IV of the kappa type (Bence-Jones protein Len1.1)";
RN Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
[2]
RN REVISION TO 9.
RP Salomon A.;
RA Submitted (AUG-1996) to the SWISS-PROT data bank.
RL MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1EEQ; 01-FEB-01.
DR PDB; 1EEU; 03-FEB-01.
DR PDB; 1EFQ; 09-FEB-01.
DR PDB; 1EK3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 5LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
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Query Match 100.0%; Score 32; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY : FTLTISS 7
DB : FTLTISS 83
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RESULT 14
KV31_HUMAN STANDARD; PRT; 115 AA.
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
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or send an email to license@isb-sib.ch).
DR EMBL; X01668; -, NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
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CC
DR EMBL; X01668; -, NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-II REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A175555 CRC64;
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Query Match 100.0%; Score 32; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLTISS 7
DB 91 FTLTISS 97
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RESULT 15
KV31_HUMAN STANDARD; PRT; 116 AA.
ID KV31_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
DR EMBL; X02725; -, NOT_ANNOTATED_CDS.
DR PIR; A01901; K3HUVH.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
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DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG\_Like; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 56 70 FRAMEWORK-2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 109 FRAMEWORK-3.  
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12757 MW; 510D55BA53B21929 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7  
Db 92 FTLTISS 98

Search completed: October 4, 2003, 12:22:36  
Job time : 11.6667 secs

GerCore version 5.1.6  
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:13 ; Search time 49.6667 Seconds  
(without alignments)  
36,370 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTISS 7

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phase:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	107	4	Q96SA9 homo sapien
2	32	100.0	107	1	Q9ERZ9 mus musculu
3	32	100.0	105	4	Q9UL83 homo sapien
4	32	100.0	103	4	Q9UL70 homo sapien
5	32	100.0	102	4	Q9UL77 homo sapien
6	32	100.0	109	4	Q9UL85 homo sapien
7	32	100.0	234	4	Q8NEK1 homo sapien
8	30	93.8	320	16	Q8FFC5 escherichia
9	30	93.8	378	5	Q8MZH9 drosophila
10	30	93.8	1004	17	Q28412 archaeoglob
11	29	90.6	108	1	Q8VJ30 mus musculu
12	29	90.6	116	4	Q36PF6 homo sapien
13	29	90.6	168	16	Q8YLY8 anabaena sp
14	29	90.6	171	12	Q69504 human herpe
15	29	90.6	195	12	Q9J0S8 rice tungro
16	29	90.6	195	12	Q9J0T0 rice tungro

17	29	90.6	196	12	Q9J0T7	Q9J0T7 rice tungro
18	29	90.6	196	12	Q9J0T2	Q9J0T2 rice tungro
19	29	90.6	196	12	Q9J0T8	Q9J0T8 rice tungro
20	29	90.6	203	12	Q9J0T4	Q9J0T4 rice tungro
21	29	90.6	203	12	Q9J0T6	Q9J0T6 rice tungro
22	29	90.6	204	12	Q9J0T5	Q9J0T5 rice tungro
23	29	90.6	205	12	Q9J0S9	Q9J0S9 rice tungro
24	29	90.6	206	12	Q9J0T9	Q9J0T9 rice tungro
25	29	90.6	206	12	Q9J0U0	Q9J0U0 rice tungro
26	29	90.6	206	12	Q9INS0	Q9INS0 rice tungro
27	29	90.6	206	12	Q9INS2	Q9INS2 rice tungro
28	29	90.6	206	12	Q9INS7	Q9INS7 rice tungro
29	29	90.6	206	12	Q9INR1	Q9INR1 rice tungro
30	29	90.6	206	12	Q9INS2	Q9INS2 rice tungro
31	29	90.6	206	12	Q9INS5	Q9INS5 rice tungro
32	29	90.6	206	12	Q9INS6	Q9INS6 rice tungro
33	29	90.6	206	12	Q9INS3	Q9INS3 rice tungro
34	29	90.6	206	12	Q9J0T3	Q9J0T3 rice tungro
35	29	90.6	206	12	Q9INR6	Q9INR6 rice tungro
36	29	90.6	206	12	Q9INR9	Q9INR9 rice tungro
37	29	90.6	206	12	Q9J0S7	Q9J0S7 rice tungro
38	29	90.6	206	12	Q9INR7	Q9INR7 rice tungro
39	29	90.6	206	12	Q9INR4	Q9INR4 rice tungro
40	29	90.6	206	12	Q9INS4	Q9INS4 rice tungro
41	29	90.6	206	12	Q9J0T1	Q9J0T1 rice tungro
42	29	90.6	206	12	Q9INS5	Q9INS5 rice tungro
43	29	90.6	206	12	Q9INR8	Q9INR8 rice tungro
44	29	90.6	216	17	Q9YAB6	Q9YAB6 aeropyrum p
45	29	90.6	258	5	Q8MPX6	Q8MPX6 culachnus r

ALIGNMENTS

RESULT :  
Q96SA9 PRELIMINARY; PRT; 107 AA.  
ID Q96SA9  
AC Q96SA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain  
DE variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin  
RT antibody V region genes";  
RJ J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 107  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;  
Query Match. 100.0%; Score 32; DB 4; Length 107;  
Best local Similarity 100.0%; Pred. No. 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : FTLTISS 7  
| | | | |  
Db 71 FTLTISS 77



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RESULT 2
Q9ERZ9          PRELIMINARY;          PRT; 107 AA.
ID Q9ERZ9
AC Q9ERZ9;
DE 01-MAR-2000 (TrEMBLrel. 16, Created)
DE 01-MAR-2000 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2000 (TrEMBLrel. 23, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-TNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -.
DR HSSP; P8C362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
DB 74 FTLTISS 50

RESULT 3
Q9UL83          PRELIMINARY;          PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DE 01-MAY-2000 (TrEMBLrel. 13, Created)
DE 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
DB 71 FTLTISS 77

RESULT 5
Q9UL77          PRELIMINARY;          PRT; 108 AA.
ID Q9UL77
AC Q9UL77;
DE 01-MAY-2000 (TrEMBLrel. 13, Created)
DE 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
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NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
"Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
Clin. Immunol. Immunopathol. 87:184-192(1998).  
EMBL; AF035037; AAD56273.1; -  
HSSP; P01607; IRE1.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS50835; IG\_LIKE; 1.  
NON\_TER 1  
NON\_TER 108  
SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
Query Match 100.0%; Score 32; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLTISS 7  
| | | | |  
Db 71 FTLTISS 77

RESULT 6  
Q9UL85 PRELIMINARY; PRT; 109 AA.  
AC Q9UL85;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin kappa chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
"Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
Clin. Immunol. Immunopathol. 87:184-192(1998).  
EMBL; AF035029; AAD56265.1; -  
HSSP; P80362; IWT.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS50835; IG\_LIKE; 1.  
NON\_TER 1  
NON\_TER 109  
SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;  
Query Match 100.0%; Score 32; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
| | | | |  
b 71 FTLTISS 77  
RESULT 7

Q8NEK1 PRELIMINARY; PRT; 234 AA.  
AC Q8NEK1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBRC databases.  
DR EMBL; BC033813; AAH30813.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25530 MW; 6316E3DEF8D132F8 CRC64;  
Query Match 100.0%; Score 32; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
| | | | |  
Db 91 FTLTISS 97

RESULT 8  
Q8FFC5 PRELIMINARY; PRT; 320 AA.  
AC Q8FFC5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein yfeN.  
GN YFE OR C2941.  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
NCBI\_TaxID=217992;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=06:H1 / CFT073 / ATCC 700928;  
RX MEDLINE=22388234; PubMed=12471157;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
of uropathogenic Escherichia coli.";  
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
DR EMBL; AE016764; AAN81391.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 320 AA; 37039 MW; EEB33B2E3811DF CRC64;  
Query Match 93.8%; Score 30; DB 16; Length 320;  
Best Local Similarity 85.7%; Pred. No. 61;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
| | | | |  
Db 72 FTLTISS 78

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SQ SEQUENCE 1004 AA; 115036 MW; 10DB5A7A3E900F6B CRC64;

Query Match      93.8%; Score 30; DB 17; Length 1004;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
DB 402 FTLTISS 408

RESULT 11
Q8VIJ0
ID Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Galkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233 (1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_VHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DE8BE CRC64;

Query Match      90.6%; Score 29; DB 11; Length 108;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
DB 71 FTLTISS 77

RESULT 12
Q86PF6
ID Q86PF6 PRELIMINARY; PRT; 116 AA.
AC Q86PF6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
contributions of Ig V(L) germ line gene use and clonal plasma cell
burden.";
RL Blood 98:714-720 (2001).

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:26 ; Search time 60.3333 Seconds  
(without alignments)  
18.416 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FASTISS 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107563 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	32	17 AAR87043	Human group I light
2	32	100.0	32	20 AAY52745	Humanised ATR-5 L
3	32	100.0	32	22 AAR98286	Anti-A33 antigen i
4	32	100.0	32	22 AAB98288	Anti-A33 antigen i
5	32	100.0	32	22 AAB97656	A33 antigen bindin
6	32	100.0	32	22 AAB97669	A33 antigen bindin
7	32	100.0	32	23 AAG98287	Human antibody 012
8	32	100.0	32	23 ABP62658	Human immunopeptid
9	32	100.0	32	23 ABP62673	Human immunopeptid

10	32	100.0	32	23 ABP62688	Human immunopeptid
11	32	100.0	32	23 AAO17650	Human PAPalpa spe
12	32	100.0	32	23 AAE19672	Human group 1 cons
13	32	100.0	32	23 AAU70396	Human light chain
14	32	100.0	32	23 AAU70408	Human light chain
15	32	100.0	32	23 AAU70436	Mouse light chain
16	32	100.0	32	23 ABG98288	Human antibody DEN
17	32	100.0	42	23 ABG98290	Human antibody Padlar VL
18	32	100.0	42	23 ABG98294	Human antibody LEN
19	32	100.0	42	23 ABG98296	Antibody Padlan VL
20	32	100.0	50	23 ABG30482	Human anti-CD40 mo
21	32	100.0	74	15 AAR62921	Human cytomagalov
22	32	100.0	74	19 AAW62805	Amino acid sequenc
23	32	100.0	75	15 AAR62923	Human cytomagalov
24	32	100.0	76	20 AAW62981	Variable kappa lig
25	32	100.0	80	24 ABG74720	Marine humanised M
26	32	100.0	82	19 AAW62807	Amino acid sequenc
27	32	100.0	84	17 AAW14491	Monoclonal antibod
28	32	100.0	84	17 AAR98878	Monoclonal antibod
29	32	100.0	86	19 AAW62806	Amino acid sequenc
30	32	100.0	88	19 AAW59619	Anti-RSV F protein
31	32	100.0	88	21 AAY56654	Partial peptide fr
32	32	100.0	88	21 AAY56655	Partial peptide fr
33	32	100.0	88	21 AAY56656	Partial peptide fr
34	32	100.0	88	21 AAY56657	Partial peptide fr
35	32	100.0	88	21 AAY56658	Partial peptide fr
36	32	100.0	88	21 AAY56659	Partial peptide fr
37	32	100.0	88	21 AAY56672	Partial peptide fr
38	32	100.0	92	23 ABG77143	Anti-IGF-IR antibo
39	32	100.0	93	23 AAO80983	Human antibody lig
40	32	100.0	94	19 AAW62808	Amino acid sequenc
41	32	100.0	94	22 AAB67510	Light chain variab
42	32	100.0	95	13 AAR28741	Light chain variab
43	32	100.0	95	15 AAR57478	Human K02 VL. Ho
44	32	100.0	95	16 AAR72061	OF7K.11 VK-1 L cha
45	32	100.0	95	16 AAR72062	OF7K.9 VK-1 L cha

ALIGNMENTS

RESULT 1  
AAR87043  
ID AAR87043 standard; Peptide; 32 AA.  
XX  
AC AAR87043;  
XX  
D7 25-JUN-1996 (first entry)  
XX  
DE Human group I light chain framework 3.  
XX  
KW Humanised antibody; interleukin-5; IL-5; recombinant antibody;  
KW antibody engineering; monoclonal antibody; MAb; 39D10; CDR;  
KW complementarity determining region; light chain; framework;  
KW eosinophilia; allergy; asthma.  
XX  
OS Homo sapiens.  
XX  
PN WO9535375-A1.  
XX  
PD 28-DEC-1995.  
XX  
PF 16-JUN-1995; 95WO-GB01411.  
XX  
PR 17-JUN-1994; 94GB-0012230.  
XX  
PA (CLLT ) CELLTECH THERAPEUTICS LTD.  
XX  
P1 Athwal DS, Bodmer MW, Emtage JS;  
XX  
DR WPI; 1996-058412/06.  
XX  
PT Anti-human IL-5 recombinant antibody - useful for preventing or

PT reducing eosinophilia and for treating certain allergic diseases,  
PT esp. asthma  
XX  
PS Example 3; Fig 3; 69pp; English.  
XX

CC Framework regions (AAR87041-44) of human group 1 (gp1) germ line  
CC antibody light chain showed homology to corresponding regions  
CC (AAR87045-48, respectively) of the rat anti-human interleukin-5  
CC monoclonal antibody 39D10 light chain (see AAR87046). This homology  
CC was utilised in the prodn. of a humanised 39D10 VL (AAR87057) in  
CC which rat 39D10 VL complementarity determining regions were grafted  
CC into the human gp1 framework.  
XX  
SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 17; Length 32;

Best Local Similarity 100.0%; Pred. No. 4.6; Length 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
|||  
DB 15 FTLTISS 21

RESULT 2  
AAY52745  
ID AAY52745 standard; Peptide; 32 AA.  
XX  
AC AAY52745;  
XX  
DT 26-JAN-2000 (first entry)  
XX  
DE Humanised ATR-5 L chain V region PR3 for a.

XX  
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;  
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;  
KW disseminated intravascular coagulation; immunogenicity; chimeric.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9951743-A1.  
XX  
PD 14-OCT-1999.  
XX  
PF 02-APR-1999; 99WO-JP01768.  
XX  
PR 03-APR-1999; 98JP-0091850.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Sato K, Adachi H, Yabuta N;  
XX  
DR WPI; 1999-620204/53.

PT Humanised antibody recognizing human tissue factor, used for treatment  
PT of disseminated intravascular coagulation -  
XX  
PS Claim 17; Page 270; 291pp; Japanese.  
XX

CC The present invention describes chimeric antibody (Ab) heavy (H) chains  
CC containing the variable region of the H chain of a mouse monoclonal Ab  
CC recognising human tissue factor (hTF) and the constant region of the H  
CC chain of a human Ab. The variable region is one of six specified  
CC sequences (which are the H chain variable regions from mouse monoclonal  
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)  
CC chains containing the variable region of the L chain of a mouse  
CC monoclonal Ab recognising human tissue factor (hTF) and the constant  
CC region of the L chain of a human Ab, the variable region being one of six  
CC specified sequences (which are the L chain variable regions from mouse  
CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for  
CC the treatment and prevention of thrombotic disease, especially of  
CC disseminated intravascular coagulation (DIC). The humanised antibody has

CC the high hTF binding activity of the mouse monoclonal antibody but  
CC greatly reduced immunogenicity. AAY33001 to AAY33091 and Y527007 to  
CC AAY52767 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 20; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
|||  
DB 15 FTLTISS 21

RESULT 3  
AAB98286  
ID AAB98286 standard; Peptide; 32 AA.  
XX  
AC AAB98286;  
XX  
DT 20-AUG-2001 (first entry)  
XX  
DE Anti-A33 antigen immunoglobulin VL PR3 SEQ ID NO:92.

XX  
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
KW immunoglobulin; complementarity determining region; CDR; cancer;  
KW cytostatic; anticancer; colon cancer; stomach cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200130393-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29289.  
XX  
PR 22-OCT-1999; 99JS-0425638.  
PR 04-APR-2000; 2000JS-0543004.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
PA (SCR ) SCRIPPS RES INST.

XX  
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
XX  
DR WPI; 2001-328613/34.  
XX

PT Treating cancers, particularly of stomach and colon, that express A33  
PT antigen by administering conjugate of anticancer agent with specific  
PT immunoglobulin product -  
XX  
PS Claim 16; Page 40; 85pp; English.  
XX

CC The present invention describes a method for treating cancers that  
CC express the A33 antigen. The method comprises administering an  
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that  
CC binds specifically to A33 and contains one or more of 13 specified  
CC complementarity determining regions (CDRs), given in AAB98262 to  
CC AAB98274. (I) has cytostatic activity. The method can be used for  
CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
CC it, can be used directly, in unconjugated form, for immunotherapy of  
CC cancer, and, when labeled, for detection or diagnosis of diseases  
CC associated with A33 expression. AAB22218 to AAB22254 and AAB98230 to  
CC AAB98321 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 FTLTISS 7
      1111111
Db      15 FTLTISS 21

RESULT 4
AAB98288
ID      AAB98288 standard; Peptide; 32 AA.
XX
AC      AAB98288;
XX
XX      20-AUG-2001 (first entry);
XX
DE      Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
XX
XX      Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW      immunoglobulin; complementarity determining region; CDR; cancer;
KW      cytostatic; anticancer; colon cancer; stomach cancer.
XX
OS      Homo sapiens.
XX
XX      WO200130393-A2.
XX
XX      03-MAY-2001.
XX
PF      20-OCT-2000; 2000WO-US29289.
XX
XX      22-OCT-1999; 99US-0425638.
XX
PR      04-APR-2000; 2000US-0543004.
XX
XX      (LUDW-) LUDWIG INST CANCER RES.
PA
PA      (SLOK) SLOAN KETTERING INST CANCER RES.
PA
XX      (SCRIP) SCRIPPS RES INST.
PI
PI      Barbas CF, Rader C, Rutter G, Weit S, Old LJ;
XX
XX      WPI; 2001-328633/34.
XX
XX      Treating cancers, particularly of stomach and colon, that express A33
PT      antigen by administering conjugate of anticancer agent with specific
PT      immunoglobulin product -
XX
PS      Claim 16; Page 40; 85pp; English.
XX
XX      The present invention describes a method for treating cancers that
CC      express the A33 antigen. The method comprises administering an
CC      anticancer agent (I) conjugated to an immunoglobulin product (II) that
CC      binds specifically to A33 and contains one or more of 13 specified
CC      complementarity determining regions (CDRs), given in AAB98262 to
CC      AAB98274. (I) has cytostatic activity. The method can be used for
CC      treating colon and stomach cancers. (II), or the nucleic acid encoding
CC      it, can be used directly, in unconjugated form, for immunotherapy of
CC      cancer, and, when labeled, for detection or diagnosis of diseases
CC      associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC      AAB98321 represent sequences used in the exemplification of the
CC      present invention.
XX
SQ      Sequence 32 AA;

Query Match 100.0%; Score 32; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
      1111111
Db      15 FTLTISS 21

RESULT 5
AAB97666
ID      AAB97666 standard; Peptide; 32 AA.
XX
XX
XX      08-AUG-2001 (first entry)
XX
DE      A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.
XX
XX      Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW      immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
OS      Homo sapiens.
XX
XX      WO200131065-A1.
XX
XX      03-MAY-2001.
XX
PF      20-OCT-2000; 2000WO-US29026.
XX
XX      22-OCT-1999; 99US-0425638.
XX
PR      04-APR-2000; 2000US-0543004.
XX
XX      (SCRIP) SCRIPPS RES INST.
PA
PA      Barbas CF, Rader C;
XX
XX      WPI; 2001-328657/34.
XX
XX      Preparing humanized rabbit antibodies that specifically immunoreact
PT      with a particular antigen using display technology for expressing
PT      libraries of antibody domains and fine tuning variable domain regions -
XX
PS      Example 9; Page 39; 62pp; English.
XX
XX      The present invention describes a method for preparing a humanised rabbit
CC      antibody that specifically immunoreacts with a particular antigen. The
CC      method comprises expressing a library of antibodies comprising one or
CC      more complementarity determining region (CDR) from the variable domain
CC      sequences that specifically immunoreact with the antigen grafted into
CC      framework regions from humans, and selecting the antibodies that react
CC      with the antigen. The method is useful for humanising non-human
CC      mammalian antibodies, which can be used for the treatment of a variety
CC      of diseases. The present sequence represents an A33 antigen binding
CC      immunoglobulin product VLFR3 peptide which is given in an example from
CC      the present invention.
XX
SQ      Sequence 32 AA;

Query Match 100.0%; Score 32; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
      1111111
Db      15 FTLTISS 21

RESULT 6
AAB97668
ID      AAB97668 standard; Peptide; 32 AA.
XX
XX
XX      AAB97668;
XX
XX      08-AUG-2001 (first entry)
XX
DE      A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.
XX
XX      Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW      immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
OS      Homo sapiens.
XX
XX      WO200131065-A1.
XX
XX      03-MAY-2001.
XX
```



XX 20-OCT-2000; 2000WO-US29026.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543304.  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Barbas CF, Rader C;  
XX W21; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing  
PT libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 9; Page 39; 62pp; English.  
XX  
XX The present invention describes a method for preparing a humanised rabbit  
CC antibody that specifically immunoreacts with a particular antigen. The  
CC method comprises expressing a library of antibodies comprising one or  
CC more complementarity determining region (CDR) from the variable domain  
CC sequences that specifically immunoreact with the antigen grafted into  
CC framework regions from humans, and selecting the antibodies that react  
CC with the antigen. The method is useful for humanising non-human  
CC mammalian antibodies, which can be used for the treatment of a variety  
CC of diseases. The present sequence represents an A13 antigen binding  
CC immunoglobulin product VLFR3 peptide which is given in an example from  
CC the present invention.  
XX  
XX Sequence 32 AA;  
SQ  
Query Match 100.0%; Score 32; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLTSS 7  
DB 15 FTLTSS 21  
RESULT 7  
ABG98287  
ID ABG98287 standard; Peptide: 32 AA.  
XX AC ABG98287;  
XX 08-JAN-2003 (first entry)  
XX Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.  
DE  
XX Antibody; variable region; light chain; heavy chain; VH; VL; gp39;  
XX CD40; T-cell activation; B-cell differentiation; framework region;  
KW cellular immune response; gene therapy; graft rejection; human; FR;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;  
KW asthma; multiple sclerosis; allergy; diabetes mellitus;  
KW systemic lupus erythematosus; graft-versus-host disease.  
XX  
XX Homo sapiens.  
OS  
XX WO200194586-A2.  
PN  
XX 13-DEC-2001.  
XX  
XX 06-JUN-2001; 2001WO-US:8099.  
PF  
XX 06-JUN-2000; 2000US-209584P.  
PR  
XX (IDEC-) IDEC PHARM CORP.  
PA  
XX Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;  
XX WPI; 2002-188261/24.  
XX

XX New antibodies binding to an epitope on gp39, useful for preventing  
PT graft rejection, or for treating autoimmune diseases (e.g. diabetes,  
PT asthma or multiple sclerosis), and non-autoimmune diseases (e.g.  
PT graft-versus-host disease) -  
XX  
XX Disclosure; Page 46; 130pp; English.  
XX  
XX The invention relates to an antibody which binds to an epitope on gp39,  
CC is new, where the epitope is distinct from the epitope bound by IDEC-131,  
CC and the antibody has a non-agonistic effect on T-cell activation and  
CC inhibits gp39/CD40 interaction. Also included are: (1) an improved method  
CC of treating a disease by modulating gp39 expression or inhibiting the  
CC gp39/CD40 interaction comprising administering an antibody specific for  
CC gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of  
CC T-cell activation; (2) an antibody which antagonises B-cell  
CC differentiation and antibody production, and is non-agonistic of T-cell  
CC activation; (3) a DNA sequence which encodes an antibody defined above;  
CC (4) an expression vector, which contains a DNA sequence of (3);  
CC (5) a method of suppressing humoral and/or cellular immune responses  
CC against cells or vectors administered during cell or gene therapy  
CC comprising further administering prior, during or after gene therapy,  
CC an antibody defined above; and (6) an improved method of treatment which  
CC involves the transplantation of cells, tissues or organs of the same or  
CC different species into a subject, where the improvement comprises  
CC administering an antibody defined above prior, during or after  
CC transplantation, to suppress immune responses against the transplanted  
CC cell, tissue or organ, or to suppress immune responses elicited by the  
CC transplanted cell, tissue or organ against the host. The antibody is  
CC useful for preventing graft rejection, and for treating autoimmune  
CC diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes,  
CC asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or  
CC systemic lupus erythematosus, as well as non-autoimmune diseases such as  
CC graft-versus-host disease (many other diseases and conditions are  
CC given in the specification). The antibodies are also useful in gene or  
CC cellular therapy, and to inhibit humoral and cellular immune responses  
CC against viral vectors. The present sequence is a framework region  
CC (FR) fragment of a human anti-gp39 antibody used to determine which  
CC amino acids should be humanised in a mouse anti-gp39 molecule.  
XX  
XX Sequence 32 AA;  
SQ  
Query Match 100.0%; Score 32; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLTSS 7  
DB 15 FTLTSS 21  
RESULT 8  
ABP62658  
ID ABP62658 standard; Peptide: 32 AA.  
XX AC ABP62658;  
XX 10-OCT-2002 (first entry)  
DT  
XX Human immunopeptide to HCV E2 glycoprotein framework sequence #166.  
DE  
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.  
XX  
XX Homo sapiens.  
CS  
XX WO200259340-A1.  
PN  
XX 01-AUG-2002.  
PD  
XX 25-CAN-2002; 2002WO-US02303.  
PF  
XX



PR 26-JAN-2001; 2001US-264451P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA Maruyama T, Jones IM, Burton DR, Fox RI;  
 PI WPI; 2002-599801/64.  
 DR New human immunopolypeptide with binding specificity for certain  
 XX envelope glycoproteins and nonstructural proteins of hepatitis C virus  
 PT (HCV), for diagnosing or treating patients having or suspected of  
 PT having HCV infection -  
 XX Claim 4; Fig 17; 308pp; English.  
 PS The present invention relates to human immunopolypeptides, produced by a  
 XX phage transfected cell library. The present sequence is one such  
 CC immunopolypeptide. The immunopolypeptides have binding specificity for  
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
 CC cell binding and contains neutralising epitopes, while NS3 is thought to  
 CC be involved in the replication of HCV. The immunopolypeptides are useful  
 CC for diagnosing and treating a patient having or suspected to be having  
 CC HCV infection.  
 XX Sequence 32 AA;  
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTISS 7  
 Db |||||  
 15 FTLTISS 21

RESULT 9  
 ABP62673  
 ID ABP62673 standard; Peptide; 32 AA.  
 XX  
 AC ABP62673;  
 DT 10-OCT-2002 (first entry)  
 XX Human immunopeptide to HCV E2 glycoprotein framework sequence #181.  
 DE Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
 KW NS3 protein; viral infection.  
 XX Homo sapiens.  
 OS WO200259340-A1.  
 XX 01-AUG-2002.  
 PD 25-JAN-2002; 2002WO-US02303.  
 PF 26-JAN-2001; 2001US-264451P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA Maruyama T, Jones IM, Burton DR, Fox RI;  
 PI WPI; 2002-599801/64.  
 DR New human immunopolypeptide with binding specificity for certain  
 XX envelope glycoproteins and nonstructural proteins of hepatitis C virus  
 PT (HCV), for diagnosing or treating patients having or suspected of  
 PT having HCV infection -  
 XX Claim 4; Fig 17; 308pp; English.

CC The present invention relates to human immunopolypeptides, produced by a  
 CC phage transfected cell library. The present sequence is one such  
 CC immunopolypeptide. The immunopolypeptides have binding specificity for  
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
 CC cell binding and contains neutralising epitopes, while NS3 is thought to  
 CC be involved in the replication of HCV. The immunopolypeptides are useful  
 CC for diagnosing and treating a patient having or suspected to be having  
 CC HCV infection.  
 XX Sequence 32 AA;  
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTISS 7  
 Db |||||  
 15 FTLTISS 21

RESULT 10  
 ABP62685  
 ID ABP62685 standard; Peptide; 32 AA.  
 XX  
 AC ABP62685;  
 DT 10-OCT-2002 (first entry)  
 XX Human immunopeptide to HCV E2 glycoprotein framework sequence #196.  
 DE Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
 KW NS3 protein; viral infection.  
 XX Homo sapiens.  
 OS WO200259340-A1.  
 XX 01-AUG-2002.  
 PD 25-JAN-2002; 2002WO-US02303.  
 PF 26-JAN-2001; 2001US-264451P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA Maruyama T, Jones IM, Burton DR, Fox RI;  
 PI WPI; 2002-599801/64.  
 DR New human immunopolypeptide with binding specificity for certain  
 XX envelope glycoproteins and nonstructural proteins of hepatitis C virus  
 PT (HCV), for diagnosing or treating patients having or suspected of  
 PT having HCV infection -  
 XX Claim 4; Fig 17; 308pp; English.  
 PS The present invention relates to human immunopolypeptides, produced by a  
 XX phage transfected cell library. The present sequence is one such  
 CC immunopolypeptide. The immunopolypeptides have binding specificity for  
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
 CC cell binding and contains neutralising epitopes, while NS3 is thought to  
 CC be involved in the replication of HCV. The immunopolypeptides are useful  
 CC for diagnosing and treating a patient having or suspected to be having  
 CC HCV infection.  
 XX Sequence 32 AA;  
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 FTLTSS 7	DT	31-MAY-2002 (first entry)	XX	
DB	15 FTLTSS 21	DE	Human group 1 consensus peptide #3.	XX	
RESULT 11		KW	Human; tumour necrosis factor 40; TNF40; osteopathic; cardiac; CDR;		
AA017650		KW	complementarity determining region; rheumatoid; osteo-arthritis; sepsis;		
ID	AAC17650 standard; Peptide; 32 AA.	KW	congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;		
XX		KW	Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;		
AC		KW	cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;		
XX		KW	inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;		
XX		XX	neoplasty therapy; immunomodulator; vilarary; graft rejection.		
DT	08-AUG-2002 (first entry)	CS	Homo sapiens.		
DE	Human FAPalpha specific V5 region from VLI143 PR3 peptide.	PN	WO200194585-A1.		
XX		XX	13-DEC-2001.		
KW	Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;	XX	05-JUN-2001; 2001WO-GE02477.		
KW	gene therapy; cancer; wound healing; inflammation; cytostatic.	PR	06-JUN-2000; 2000GB-0013810.		
OS	Homo sapiens.	XX	(CELL-) CELUTECH R & D LTD.		
XX		PA	Athwal DS, Brown DT, Weir ANC, Poppewell AG, Chapman AF, King DC;		
PN	WO200168708-A2.	PI	WEI; 2002-216732/27.		
PD	20-SEP-2001.	XX	New antibody specific for human tumor necrosis factor (TNF)-alpha,		
XX	16-MAR-2001; 2001WO-BPC4716.	XX	useful for treating TNF-alpha-mediated diseases, e.g. congestive heart		
PF	17-MAR-2000; 2000DE-1013286.	PT	failure, septic or endotoxic shock, cachexia, adult respiratory		
XX	11-SEP-2000; 2000GB-0022216.	PT	distress syndrome		
PR	(BOEH) BOEHRINGER INGELHEIM PHARMA KG.	XX	Example 1; Fig 1; 119pp; English.		
XX		PS	The invention relates to an antibody molecule having specificity for		
PA	Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;	CC	human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light		
PI	Schmidt A;	CC	chain. The antibody or the compound comprising the antibody is useful		
XX		CC	for treating or manufacturing a medicament for treating a pathology		
DR	WPI; 2002-041190/05.	CC	mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha		
DR	N-PSDB; AAL46595.	CC	mediated diseases which can be treated by the antibody include sepsis,		
XX	New human humanized antibody that specifically binds to fibroblasts	CC	congestive heart failure, septic or endotoxic shock, cachexia, adult		
PT	activating protein alpha, useful for treating cancer or tumor, and for	CC	respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),		
PT	imaging tumors associated with activated stromal fibroblasts, e.g. lung	CC	allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood		
PT	or breast cancer	CC	coagulation disorders, burns, rejection episodes following organ or		
XX		CC	tissue transplant, Crohn's disease and autoimmune diseases, such as		
PS	Disclosure; Fig 6H; 109pp; English.	CC	thyroiditis. The antibodies may also be used to reduce the side effects		
XX		CC	associated with TNFalpha generation during neoplasty therapy, to		
CC	The present invention relates to a human or humanised antibody (Ab) which	CC	eliminate or reduce shock-related symptoms associated with the treatment		
CC	specifically binds to fibroblast activating protein alpha (FAPalpha). The	CC	or prevention of graft rejection by use of an anti-lymphocyte antibody,		
CC	antibodies are useful for preparing a composition for the treatment of	CC	for treating multi-organ failure, or in the diagnosis and imaging of		
CC	cancer, and for imaging tumours associated with activated stromal	CC	disease states involving elevated levels of TNF alpha. The present		
CC	fibroblasts, such as colorectal cancer, non-small-cell lung cancer,	CC	sequence is human group 1 consensus peptide used in the exemplification		
CC	breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder	XX	of the invention.		
CC	cancer, pancreatic cancer and metastatic brain cancer, and diseases	SQ	Sequence 32 AA;		
CC	associated with the same, such as inflammation and wound healing. The		Query Match 100.0%; Score 32; DB 23; Length 32;		
CC	present sequence is a peptide described in the exemplification of the		Best Local Similarity 100.0%; Pred. NO. 4.6;		
XX			Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 FTLTSS 7	QY	1 FTLTSS 7		
DB	15 FTLTSS 21	DB	15 FTLTSS 21		
RESULT 12		RESULT 13			
AAE19672		AAU70396			
ID	AAE19672 standard; peptide; 32 AA.	ID	AAU70396 standard; Peptide; 32 AA.		
XX		XX			
AC		AC	AAU70396;		
XX		DT	14-FEB-2002 (first entry)		

XX DE Human light chain immunoglobulin framework region 3 #1.  
XX XX  
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array;  
KW IGM; IGG; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHBP.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX FN WO200193806-A1.  
XX XX  
XX PD 08-NOV-2001.  
XX XX  
XX PF 02-MAY-2001; 2001WO-US14349.  
XX XX  
XX PR 02-MAY-2000; 2000US-0563222.  
XX XX  
XX PA (EPIC-) EPICYTE PHARM INC.  
XX PI Hiatt AC, Hein MB;  
XX XX  
XX DR WPI; 2002-055482/07.  
XX XX  
XX PT Preparing immunoglobulin binding protein array in plant cells by  
XX PT transforming the cells with different polynucleotides encoding binding  
XX PT protein polypeptides specific to ligand, selecting plant cells for  
XX PT preparing array -  
XX XX  
XX PS Disclosure; Fig 1A; 129pp; English.  
XX XX  
XX CC The invention relates to transforming a population of cells (e.g. plant  
XX CC cells), comprising using a library of two different polynucleotides  
XX CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
XX CC that specifically bind to a ligand or form one or more disulphide bonds  
XX CC with polypeptides in transfected cells, to generate an IgBP that  
XX CC binds to a ligand, and transformed plant cells are selected, and  
XX CC preparing an IgBP array in plant cells. At least one peptide sequence has  
XX CC at least 75% sequence identity to a framework region (FR) of a native  
XX CC IGM, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.  
XX CC The method is useful for preparing an immunoglobulin binding protein  
XX CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
XX CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
XX CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
XX CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
XX CC desired characteristics. The present sequence is a mammalian  
XX CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
XX CC the invention.  
XX XX  
XX SQ Sequence 32 AA;  
Query Match 100.0%; Score 32; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 FTLTSS 7  
| | | | |  
Db 15 FTLTSS 21

RESULT 14  
AAU70408  
ID AAU70408 standard; Peptide; 32 AA.  
XX XX  
XX AC AAU70408;  
XX XX  
XX DT 14-FEB-2002 (first entry)  
XX XX  
XX DE Human light chain immunoglobulin framework region 3 #4.  
XX XX  
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
XX KW complementarity determining region; framework region; IgBP;  
XX KW transgenic plant; immunoglobulin binding protein array;

KW IGM; IGG; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHBP.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX FN WO200183806-A1.  
XX XX  
XX PD 08-NOV-2001.  
XX XX  
XX PF 02-MAY-2001; 2001WO-US14349.  
XX XX  
XX PR 02-MAY-2000; 2000US-0563222.  
XX XX  
XX PA (EPIC-) EPICYTE PHARM INC.  
XX XX  
XX PI Hiatt AC, Hein MB;  
XX XX  
XX DR WPI; 2002-055482/07.  
XX XX  
XX PT Preparing immunoglobulin binding protein array in plant cells by  
XX PT transforming the cells with different polynucleotides encoding binding  
XX PT protein polypeptides specific to ligand, selecting plant cells for  
XX PT preparing array -  
XX XX  
XX PS Disclosure; Fig 1A; 129pp; English.  
XX XX  
XX CC The invention relates to transforming a population of cells (e.g. plant  
XX CC cells), comprising using a library of two different polynucleotides  
XX CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
XX CC that specifically bind to a ligand or form one or more disulphide bonds  
XX CC with polypeptides in transfected cells, to generate an IgBP that  
XX CC binds to a ligand, and transformed plant cells are selected, and  
XX CC preparing an IgBP array in plant cells. At least one peptide sequence has  
XX CC at least 75% sequence identity to a framework region (FR) of a native  
XX CC IGM, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.  
XX CC The method is useful for preparing an immunoglobulin binding protein  
XX CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
XX CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
XX CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
XX CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
XX CC desired characteristics. The present sequence is a mammalian  
XX CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
XX CC the invention.  
XX XX  
XX SQ Sequence 32 AA;  
Query Match 100.0%; Score 32; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLTSS 7  
| | | | |  
Db 15 FTLTSS 21

RESULT 15  
AAU70436  
ID AAU70436 standard; Peptide; 32 AA.  
XX XX  
XX AC AAU70436;  
XX XX  
XX DT 14-FEB-2002 (first entry)  
XX XX  
XX DE Mouse light chain immunoglobulin framework region 3 #1.  
XX XX  
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
XX KW complementarity determining region; framework region; IgBP;  
XX KW transgenic plant; immunoglobulin binding protein array;  
XX KW IGM; IGG; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHBP.  
XX XX  
XX OS Mus musculus.  
XX XX  
XX PN WO200183806-A1.  
XX XX

PD 08-NOV-2001.  
XX  
XX PF 02-MAY-2001; 2001WO-US14349.  
XX  
XX PR 02-MAY-2000; 2000US-0563222.  
XX  
XX PA (EPIC-) EPICYTE PHARM INC.  
XX  
XX PI Hiatt AC, Hein MS;  
XX  
XX WPI; 2002-055482/C7.  
XX  
XX Preparing immunoglobulin binding protein array in plant cells by  
XX transforming the cells with different polynucleotides encoding binding  
XX protein polypeptides specific to ligand, selecting plant cells for  
XX preparing array -  
PS Disclosure; Fig 1A; 120pp; English.  
XX  
XX The invention relates to transforming a population of cells (e.g. plant  
XX cells), comprising using a library of two different polynucleotides  
XX encoding different immunoglobulin binding protein (IgBP) polypeptides  
XX that specifically bind to a ligand or form one or more disulphide bonds  
XX with polypeptides in transfected cells, to generate an IgBP that  
XX binds to a ligand, and transformed plant cells are selected, and  
XX preparing an IgBP array in plant cells. At least one peptide sequence has  
XX at least 75% sequence identity to a framework region (FR) of a native  
XX IGM, IGG, IGA, IGB, IGE, IGF, kappa or lambda immunoglobulin molecule.  
XX The method is useful for preparing an immunoglobulin binding protein  
XX array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
XX cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
XX or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
XX CHBP is useful for discovery of e.g. screening assays of IgBPs having  
XX desired characteristics. The present sequence is a mammalian  
XX immunoglobulin derived peptide that may be incorporated into an IgBP of  
XX the invention.  
SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
Db 15 FTLTSS 21

Search completed: October 4, 2003, 12:21:57  
Job time : 62.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:25:27 ; Search time 35.3333 Seconds  
(without alignments:  
31.344 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PTC\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PTC05\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	32	9	US-09-855-271-13 Sequence 13, Appl
2	32	100.0	32	10	US-09-828-708-95 Sequence 95, Appl
3	32	100.0	32	10	US-09-828-708-96 Sequence 96, Appl
4	32	100.0	32	10	US-09-828-708-98 Sequence 98, Appl
5	32	100.0	32	10	US-09-949-559-91 Sequence 91, Appl
6	32	100.0	32	11	US-09-874-141-15 Sequence 15, Appl
7	32	100.0	32	11	US-09-875-221A-91 Sequence 91, Appl
8	32	100.0	32	11	US-09-563-222-76 Sequence 76, Appl
9	32	100.0	32	11	US-09-563-222-88 Sequence 88, Appl
10	32	100.0	32	11	US-09-563-222-116 Sequence 116, Appl
11	32	100.0	32	12	US-10-160-506-15 Sequence 15, Appl
12	32	100.0	36	12	US-10-387-645-5 Sequence 5, Appl
13	32	100.0	42	11	US-09-874-141-16 Sequence 16, Appl
14	32	100.0	42	11	US-09-874-141-18 Sequence 18, Appl
15	32	100.0	42	11	US-09-874-141-22 Sequence 22, Appl

16	32	100.0	42	11	US-09-874-141-24 Sequence 24, Appl
17	32	100.0	70	12	US-10-171-681-9 Sequence 9, Appl
18	32	100.0	70	12	US-10-171-680-9 Sequence 9, Appl
19	32	100.0	73	15	US-10-078-958-13 Sequence 13, Appl
20	32	100.0	76	10	US-09-187-693-37 Sequence 37, Appl
21	32	100.0	80	11	US-09-269-921-130 Sequence 130, Appl
22	32	100.0	80	11	US-09-509-098-131 Sequence 131, Appl
23	32	100.0	80	12	US-10-160-506-18 Sequence 18, Appl
24	32	100.0	80	12	US-10-171-681-10 Sequence 10, Appl
25	32	100.0	80	12	US-10-171-681-12 Sequence 12, Appl
26	32	100.0	80	12	US-10-171-681-13 Sequence 13, Appl
27	32	100.0	80	12	US-10-171-681-15 Sequence 15, Appl
28	32	100.0	80	12	US-10-171-680-10 Sequence 10, Appl
29	32	100.0	80	12	US-10-171-680-12 Sequence 12, Appl
30	32	100.0	80	12	US-10-171-680-13 Sequence 13, Appl
31	32	100.0	80	12	US-10-171-680-15 Sequence 15, Appl
32	32	100.0	80	16	US-10-218-253-130 Sequence 130, Appl
33	32	100.0	81	11	US-09-910-483-40 Sequence 40, Appl
34	32	100.0	81	11	US-09-910-483-46 Sequence 46, Appl
35	32	100.0	82	15	US-10-078-958-15 Sequence 15, Appl
36	32	100.0	88	9	US-09-905-243-31 Sequence 31, Appl
37	32	100.0	88	9	US-09-905-243-32 Sequence 32, Appl
38	32	100.0	88	9	US-09-905-243-33 Sequence 33, Appl
39	32	100.0	89	9	US-09-905-243-34 Sequence 34, Appl
40	32	100.0	88	9	US-09-905-243-35 Sequence 35, Appl
41	32	100.0	88	9	US-09-905-243-36 Sequence 36, Appl
42	32	100.0	88	9	US-09-905-243-63 Sequence 63, Appl
43	32	100.0	88	14	US-10-066-895-9 Sequence 9, Appl
44	32	100.0	93	10	US-09-965-099-35 Sequence 35, Appl
45	32	100.0	93	14	US-10-051-852-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1  
US-09-855-271-13  
; Sequence 13, Application US/09855271  
; Patent No. US20020042089A1  
; GENERAL INFORMATION:  
; APPLICANT: Bodmer, Mark W  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Emtage, John Spencer  
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies  
; FILE REFERENCE: CARP-0088  
; CURRENT APPLICATION NUMBER: US/09/855,271  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/347,061  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus  
US-09-855-271-13

Query Match 100.0%; Score 32; DB 9; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7  
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Db 15 FTLTSS 21

RESULT 2  
US-09-828-708-95  
; Sequence 95, Application US/09828708  
; Patent No. US20020146753A1  
; GENERAL INFORMATION:

```
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-95

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 3
US-09-828-708-96
; Sequence 96, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-96

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 4
US-09-828-708-98
; Sequence 98, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-828-708-98

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 5
US-09-949-559-91
; Sequence 91, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework 13
US-09-949-559-91

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 6
US-09-874-141-15
; Sequence 15, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GPI9, COMPOSITIONS
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-874-141-15

Query Match 100.0%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7  
| | | | |  
Db 15 FTLTISS 21

RESULT 7

US-09-875-221A-91  
; Sequence 91, Application US/09875221A  
; Publication No. US2003026805A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahtwal, Diljeet Singh  
; APPLICANT: Brown, Derek Thomas  
; APPLICANT: Weir, Andrew Neil Charles  
; APPLICANT: Popplewell, Andrew George  
; APPLICANT: Chapman, Andrew Paul  
; APPLICANT: King, David John  
; TITLE OF INVENTION: Biological Products  
; FILE REFERENCE: Carp-0089  
; CURRENT APPLICATION NUMBER: US/09/875,221A  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: GB0013810.7  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 91  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human group 1 consensus framework L3  
US-09-875-221A-91

Query Match 100.0%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7  
| | | | |  
Db 15 FTLTISS 21

RESULT 8

US-09-563-222-76  
; Sequence 76, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-563-222-76

Query Match 100.0%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7  
| | | | |

Db 15 FTLTISS 21

RESULT 9

US-09-563-222-88  
; Sequence 88, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-563-222-88

Query Match 100.0%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7  
| | | | |  
Db 15 FTLTISS 21

RESULT 10

US-09-563-222-116  
; Sequence 116, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-116

Query Match 100.0%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7  
| | | | |  
Db 15 FTLTISS 21

RESULT 11

US-10-160-506-15  
; Sequence 15, Application US/10160506  
; Publication No. US20030161832A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
; FILE REFERENCE: 10448-162001  
; CURRENT APPLICATION NUMBER: US/10/160,506  
; CURRENT FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: 60/324,100  
PRIOR FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: 60/362,612  
PRIOR FILING DATE: 2002-03-08  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: deimmunized light chain J591  
US-10-160-506-15

Query Match 100.0%; Score 32; DB 12; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
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DB 15 FTLTSS 21

## RESULT 12

US-10-387-645-5  
Sequence 5, Application: US/10387645  
Publication No. US20030175845A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: KAUBAG, Suresh M.  
APPLICANT: KARUNATILAKE, Chulani  
TITLE OF INVENTION: USE OF SULFITYLYSIS IN HIGH PERFORMANCE  
TITLE OF INVENTION: PEPTIDE MAPPING  
FILE REFERENCE: 39766-0102A  
CURRENT APPLICATION NUMBER: US/10/387,645  
CURRENT FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 60/364,992  
PRIOR FILING DATE: 2002-03-13  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-387-645-5

Query Match 100.0%; Score 32; DB 12; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
|||  
DB 5 FTLTSS 11

## RESULT 13

US-09-874-141-16  
Sequence 16, Application: US/09874141  
Publication No. US20030012781A1  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DARRELL  
APPLICANT: PAN, LI-ZHEN  
APPLICANT: HANNA, NABIL  
APPLICANT: RASTETTER, WILLIAM H.  
APPLICANT: KLOETZER, WILLIAM S.  
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
FILE REFERENCE: 037003-0280632  
CURRENT APPLICATION NUMBER: US/09/874,141  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/209,584  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-874-141-16

Query Match 100.0%; Score 32; DB 11; Length 42;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
|||  
DB 15 FTLTSS 21

## RESULT 14

US-09-874-141-18  
Sequence 18, Application: US/09874141  
Publication No. US20030012781A1  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DARRELL  
APPLICANT: PAN, LI-ZHEN  
APPLICANT: HANNA, NABIL  
APPLICANT: RASTETTER, WILLIAM H.  
APPLICANT: KLOETZER, WILLIAM S.  
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
FILE REFERENCE: 037003-0280632  
CURRENT APPLICATION NUMBER: US/09/874,141  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/209,584  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: humanized VL#1 peptide  
US-09-874-141-18

Query Match 100.0%; Score 32; DB 11; Length 42;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
|||  
DB 15 FTLTSS 21

## RESULT 15

US-09-874-141-22  
Sequence 22, Application: US/09874141  
Publication No. US20030012781A1  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DARRELL  
APPLICANT: PAN, LI-ZHEN  
APPLICANT: HANNA, NABIL  
APPLICANT: RASTETTER, WILLIAM H.  
APPLICANT: KLOETZER, WILLIAM S.  
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
FILE REFERENCE: 037003-0280632  
CURRENT APPLICATION NUMBER: US/09/874,141  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/209,584  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22



LENGTH: 42  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-874-141-22  
Query Match 100.0%; Score 32; DB 11; Length 42;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 FRTISS 7  
Db 15 FRTISS 21

Search completed: October 4, 2003, 12:42:38  
Job time : 36.333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:18:51 ; Search time 17.6667 Seconds  
(without alignments)  
15.765 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/aaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/aaa/5R\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/aaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/aaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/aaa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/aaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	25	5	PCT-US91-02942-26 Sequence 26, Appl
2	32	100.0	25	5	PCT-US91-02942-42 Sequence 42, Appl
3	32	100.0	32	2	US-08-470-139-13 Sequence 13, Appl
4	32	100.0	32	3	US-08-569-147-40 Sequence 40, Appl
5	32	100.0	32	4	US-09-347-061-13 Sequence 13, Appl
6	32	100.0	32	4	US-09-425-638A-92 Sequence 92, Appl
7	32	100.0	32	4	US-09-425-638A-94 Sequence 94, Appl
8	32	100.0	32	4	US-08-543-004-92 Sequence 92, Appl
9	32	100.0	32	4	US-09-543-004-94 Sequence 94, Appl
10	32	100.0	50	5	PCT-US91-02942-8 Sequence 8, Appl
11	32	100.0	50	5	PCT-US91-02942-9 Sequence 9, Appl
12	32	100.0	64	2	US-08-765-179B-10 Sequence 10, Appl
13	32	100.0	64	2	US-08-765-179B-14 Sequence 14, Appl
14	32	100.0	70	3	US-08-554-840-9 Sequence 9, Appl
15	32	100.0	70	4	US-08-525-339-9 Sequence 9, Appl
16	32	100.0	70	4	US-09-332-595-9 Sequence 9, Appl
17	32	100.0	76	3	US-08-851-362D-21 Sequence 21, Appl
18	32	100.0	80	3	US-08-554-840-10 Sequence 10, Appl
19	32	100.0	80	3	US-08-554-840-12 Sequence 12, Appl
20	32	100.0	80	3	US-08-554-840-13 Sequence 13, Appl
21	32	100.0	80	3	US-08-554-840-15 Sequence 15, Appl
22	32	100.0	80	4	US-08-925-339-10 Sequence 10, Appl
23	32	100.0	80	4	US-08-925-339-12 Sequence 12, Appl
24	32	100.0	80	4	US-08-925-339-13 Sequence 13, Appl
25	32	100.0	80	4	US-08-925-339-15 Sequence 15, Appl
26	32	100.0	80	4	US-09-332-595-10 Sequence 10, Appl
27	32	100.0	80	4	US-09-332-595-12 Sequence 12, Appl

28	32	100.0	80	4	US-09-312-595-13 Sequence 13, Appl
29	32	100.0	80	4	US-09-312-595-15 Sequence 15, Appl
30	32	100.0	93	3	US-08-783-853A-35 Sequence 35, Appl
31	32	100.0	93	4	US-09-344-050-35 Sequence 35, Appl
32	32	100.0	95	2	US-08-290-592E-19 Sequence 19, Appl
33	32	100.0	95	2	US-08-290-592E-33 Sequence 33, Appl
34	32	100.0	95	5	PCT-US95-10053-16 Sequence 16, Appl
35	32	100.0	95	5	PCT-US95-10053-30 Sequence 30, Appl
36	32	100.0	95	5	PCT-US96-09448-19 Sequence 19, Appl
37	32	100.0	95	5	PCT-US96-09448-33 Sequence 33, Appl
38	32	100.0	96	3	US-08-466-368-6 Sequence 6, Appl
39	32	100.0	96	4	US-08-470-998-3 Sequence 3, Appl
40	32	100.0	99	4	US-09-899-896-6 Sequence 6, Appl
41	32	100.0	99	4	US-09-899-896-10 Sequence 10, Appl
42	32	100.0	100	4	US-09-899-896-2 Sequence 2, Appl
43	32	100.0	103	3	US-09-240-274-42 Sequence 42, Appl
44	32	100.0	104	1	US-08-276-852-106 Sequence 106, App
45	32	100.0	104	1	US-08-899-575-106 Sequence 106, App

ALIGNMENTS

RESULT 1  
PCT-US91-02942-26  
; Sequence 26, Application PC/US9102942  
; GENERAL INFORMATION:  
; APPLICANT: ROTHLEIN, ROBERT  
; APPLICANT: ADAIR, JOHN R  
; APPLICANT: ATHWAL, DILJEET S  
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Ave. NW Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02942  
; FILING DATE: 1991-04-29  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9009549.8  
; FILING DATE: 27-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAM L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 1011.0586600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US91-02942-26

Query Match 100.0% Score 32; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 8 FTLTISS 14

RESULT 2  
PCT-US91-02942-42  
; Sequence 42, Application PC/TUS9102942  
; GENERAL INFORMATION:  
; APPLICANT: ROTHLEIN, ROBERT  
; APPLICANT: ADAIR, JOHN R  
; APPLICANT: AHWAL, DILJEET S  
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Ave, NW Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02942  
; FILING DATE: 1991-04-29  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9009549.8  
; FILING DATE: 27-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAM J.  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 1011.0586600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US91-02942-42

Query Match 100.0%; Score 32; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLTSS 7  
Db 8 FTLTSS 14

RESULT 3  
US-08-470-139-13  
; Sequence 13, Application US/08470139  
; Patent No. 5998586  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies  
; NUMBER OF SEQUENCES: 28  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPC)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,139  
; FILING DATE: 06 JUNE-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TRUJILLO, DOREEN YATKO

; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0044  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-470-139-13

Query Match 100.0%; Score 32; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLTSS 7  
Db 15 FTLTSS 21

RESULT 4  
US-08-569-147-40  
; Sequence 40, Application US/08569147  
; Patent No. 6180377  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: HUMANISED ANTIBODIES  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; ADDRESSEE: No. 6180377ris, LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPC)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,147  
; FILING DATE: 25-March-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yatk  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0047  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-569-147-40

Query Match 100.0%; Score 32; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLTSS 7  
Db 15 FTLTSS 21

RESULT 5  
US-09-347-061-13  
; Sequence 13, Application US/09347061

```
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21

RESULT 6
US-09-425-638A-92
; Sequence 92, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-92

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21

RESULT 7
US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-94

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21

RESULT 8
US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-92

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21

RESULT 9
US-09-543-004-94
; Sequence 94, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21

RESULT 10
US-09-543-004-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match          100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : FTLTSS 7
         |||||
Db       15 FTLTSS 21
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PCT-US91-02942-8  
; Sequence 8, Application PC/TUS9102942  
; GENERAL INFORMATION:  
; APPLICANT: ROTHLEIN, ROBERT  
; APPLICANT: ADAIR, JOHN R  
; APPLICANT: ATHWAL, DILJEET S  
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Ave. NW Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02942  
; FILING DATE: 19910429  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9009549.8  
; FILING DATE: 27-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAM L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 1011.0586600  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US91-02942-8  
  
Query Match: 100.0%; Score 32; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLTISS 7  
DB 26 FTLTISS 32  
  
RESULT 11  
PCT-US91-02942-9  
; Sequence 9, Application PC/TUS9102942  
; GENERAL INFORMATION:  
; APPLICANT: ROTHLEIN, ROBERT  
; APPLICANT: ADAIR, JOHN R  
; APPLICANT: ATHWAL, DILJEET S  
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Ave. NW Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/02942  
; FILING DATE: 19910429  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9009549.8  
; FILING DATE: 27-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAM L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 1011.0586600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US91-02942-9  
  
Query Match: 100.0%; Score 32; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLTISS 7  
DB 26 FTLTISS 32  
  
RESULT 12  
US-08-765-179B-10  
; Sequence 10, Application US/08765179B  
; Patent No. 5854027  
; GENERAL INFORMATION:  
; APPLICANT: STEIPE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
; TITLE OF INVENTION: OF ANTIBODIES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Cram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,179B  
; FILING DATE: 14-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/02626  
; FILING DATE: 06-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 44 25 115.7  
; FILING DATE: 15-JUL-1994  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-765-179B-10  
  
Query Match: 100.0%; Score 32; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 6.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
|||||  
40 FTLTSS 46

DB

RESULT 13  
US-08-765-179B-14  
; Sequence 14, Application: US/08765179B  
; Patent No. 5854027  
; GENERAL INFORMATION:  
; APPLICANT: STRIPE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
; TITLE OF INVENTION: OF ANTIBODIES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikolaïdo, Marmelstein, Murray & Gram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/38/765,179B  
; FILING DATE: 14-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/02626  
; FILING DATE: 06-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 44 25 115.7  
; FILING DATE: 15-JUL-1994  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; S-08-765-179B-14

Query Match 100.0%; Score 32; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 FTLTSS 7  
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40 FTLTSS 46

D

RESULT 14  
S-08-554-840-9  
; Sequence 9, Application: US/08554840  
; Patent No. 6001358  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, Amelia  
; APPLICANT: HANNA, Nabil  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: NEWMAN, Roland A.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria

; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/554,840  
; FILING DATE: 07-NOV-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-127  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 70 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; S-08-554-840-9

Query Match 100.0%; Score 32; DB 3; Length 70;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7  
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53 FTLTSS 59

DB

RESULT 15  
US-08-925-339-9  
; Sequence 9, Application: US/08925339  
; Patent No. 6440418  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, Amelia  
; APPLICANT: HANNA, Nabil  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: NEWMAN, Roland A.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/925,339  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/554,840  
; FILING DATE: 07-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-127  
; TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (703) 836-6620  
/ TELEFAX: (703) 836-2021  
/ INFORMATION FOR SEQ ID NO: 9:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 70 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-08-925-339-9

Query Match 100.0%, Score 32; DB 4; Length 70;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTISS 7

Db 53 FTLTISS 59

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Job time : 18.6667 secs

GenCore version 5.1.6  
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:36 ; Search time 20.3333 Seconds  
(without alignments)  
33.107 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96163682 residues

total number of hits satisfying chosen parameters: 283305

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match: 100%  
Listing first 45 summaries

Database : PIR\_76:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	34	2 H3C607	Ig kappa chain V-I
2	35	100.0	54	2 A25521	Ig kappa chain V-I
3	35	100.0	54	2 A25521	Ig kappa chain V-I
4	35	100.0	71	2 S21526	Ig kappa chain V-I
5	35	100.0	78	2 S34102	Ig kappa chain V-I
6	35	100.0	79	2 S24215	Ig kappa chain V-I
7	35	100.0	91	2 P11C48	Ig light chain V-I
8	35	100.0	82	2 S38560	Ig light chain V-I
9	35	100.0	82	2 S34090	Ig kappa chain V-I
10	35	100.0	83	2 I3C607	Ig kappa chain V-I
11	35	100.0	86	2 S16826	Ig kappa chain V-I
12	35	100.0	86	2 S16834	Ig kappa chain V-I
13	35	100.0	86	2 S16836	Ig kappa chain V-I
14	35	100.0	86	2 S34086	Ig kappa chain V-I
15	35	100.0	86	2 S16840	Ig kappa chain V-I
16	35	100.0	86	2 S16837	Ig kappa chain V-I
17	35	100.0	86	2 S16833	Ig kappa chain V-I
18	35	100.0	86	2 S16830	Ig kappa chain V-I
19	35	100.0	86	2 S16824	Ig kappa chain V-I
20	35	100.0	86	2 S16829	Ig kappa chain V-I
21	35	100.0	87	2 S16843	Ig kappa chain V-I
22	35	100.0	87	2 S16842	Ig kappa chain V-I
23	35	100.0	87	2 S16841	Ig kappa chain V-I
24	35	100.0	87	2 S34084	Ig kappa chain V-I
25	35	100.0	87	2 S34083	Ig kappa chain V-I
26	35	100.0	88	2 S21528	Ig kappa chain V-I
27	35	100.0	88	2 S21524	Ig kappa chain V-I
28	35	100.0	88	2 S21525	Ig kappa chain V-I
29	35	100.0	88	2 S21522	Ig kappa chain V-I

30	35	100.0	89	2 S34096	Ig kappa chain V-I
31	35	100.0	90	2 S38561	Ig light chain V-I
32	35	100.0	90	2 I38601	Ig kappa chain V-I
33	35	100.0	91	2 P11C71	Ig light chain V-I
34	35	100.0	91	2 S25462	Ig kappa chain V-I
35	35	100.0	91	2 S37520	Ig kappa chain V-I
36	35	100.0	91	2 S37521	Ig kappa chain V-I
37	35	100.0	91	2 S67940	Ig kappa chain V-I
38	35	100.0	92	2 S37533	Ig kappa chain V-I
39	35	100.0	92	2 S37530	Ig kappa chain V-I
40	35	100.0	92	2 S37529	Ig kappa chain V-I
41	35	100.0	92	2 S37535	Ig kappa chain V-I
42	35	100.0	92	2 S37524	Ig kappa chain V-I
43	35	100.0	92	2 S37513	Ig kappa chain V-I
44	35	100.0	92	2 S37512	Ig kappa chain V-I
45	35	100.0	92	2 S37531	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

H3C607  
Ig kappa chain V-III region (Bia) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 30-May-1997  
C:Accession: H30607  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, F.; So  
J. Immunol. 142, 3158-3163, 1989  
A>Title: Structural and idiotypic characterization of the L chains of human IgM autoan  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: H30607  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-34 <GON>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 35; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TDFTLTI 7  
Db 23 TDFTLTI 29

RESULT 2

A25521  
Ig kappa chain V region (321) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 21-May-1988 #sequence\_revision 21-May-1990 #text\_change 09-May-1997  
C:Accession: A25521  
R:Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986  
A>Title: Genetic basis for the cross-reactive idiotypes on the light chains of human I  
A:Reference number: A94135; MUID:87041448; PMID:3095834  
A:Accession: A25521  
A:Molecule type: DNA  
A:Residues: 1-54 <CHE>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 35; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TDFTLTI 7  
Db 28 TDFTLTI 34

RESULT 3



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JT0521
Ig kappa chain V-II region (CP1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
C:Accession: JT0521
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0521; MUID:69279157; PMID:2786547
A:Accession: JT0521
A:Molecule type: mRNA
A:Residues: 1-54 <ANK>
A:Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-49/Domain: V region <VRE>
F:50-54/Domain: J region <JRE>

Query Match          100.0%; Score 35; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
    |||||
Db 21 TDFTLTI 27

RESULT 4
S21526
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C:Accession: S34082; S21526
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WA2>
A:Cross-references: EMBL:X66042; NID:G33318; PID:CAA46841.1; PID:G33319
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 35; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
    |||||
Db 62 TDFTLTI 68

RESULT 5
S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 35; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
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Db 60 TDFTLTI 66

Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
    |||||
Db 60 TDFTLTI 66

RESULT 6
S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular exc
A:Reference number: S24214; MUID:91217618; PMID:1902500
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:G53718; PID:CAA41178.1; PID:G930195
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 35; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
    |||||
Db 42 TDFTLTI 48

RESULT 7
PH1048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1048
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective E
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1048
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match          100.0%; Score 35; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
    |||||
Db 54 TDFTLTI 60

RESULT 8
S38560
Ig light chain V region (ASWB1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38560
R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A:Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s
A:Reference number: S38559
A:Accession: S38560
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <MON>
A;Cross-references: EMBL:X75102; NID:9414147; PIDN:CAA52993.1; PID:9414148
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
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Db 69 TDFTLTI 75

RESULT 9
S34090
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34090
C;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:6436174
A;Accession: S34090
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-82 <WAG>
A;Cross-references: EMBL:X67174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 35; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
    |||||
Db 60 TDFTLTI 66

RESULT 10
I30607
Ig kappa chain V-II region (Wei) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C;Accession: I30607
C;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjencia, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3152-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-83 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
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Db 70 TDFTLTI 76

RESULT 11
S16826
g kappa chain V region - human (fragment)
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C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16826; S34101
C;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16826
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54824; NID:933653; PIDN:CAA38593.1; PID:933654
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribu
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34101
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAG>
A;Cross-references: EMBL:X67185
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
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Db 60 TDFTLTI 66

RESULT 12
S16834
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C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54832
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
    |||||
Db 60 TDFTLTI 66

RESULT 13
S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
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A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-86 <BLA>  
A;Cross-references: EMBL:X54834  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLT 7  
DB 60 TDFLT 66

RESULT 14  
S34086  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S34086  
R;Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia and distributed  
A;Reference number: S34076; XJID:93170387; PMID:8436174  
A;Accession: S34086  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-86 <WAG>  
A;Cross-references: EMBL:X67169  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLT 7  
DB 62 TDFLT 68

RESULT 15  
S16840  
Ig kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S16840  
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.  
Eur. J. Immunol. 21, 1221-1227, 1991  
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac  
A;Reference number: S16823; XJID:91243737; PMID:1903706  
A;Accession: S16840  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-86 <BLA>  
A;Cross-references: EMBL:X54838  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLT 7  
DB 60 TDFLT 66

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:51 ; Search time 10.6667 Seconds  
(without alignments)  
30.861 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	100	KV3C_HUMAN	P01621 homo sapien
2	35	100.0	107	KV04_RABIT	P01695 cryptolagus
3	35	100.0	107	KV1E_HUMAN	P01596 homo sapien
4	35	100.0	108	KV06_RABIT	P01697 cryptolagus
5	35	100.0	108	KV1E_HUMAN	P01597 homo sapien
6	35	100.0	108	KV1E_HUMAN	P01600 homo sapien
7	35	100.0	108	KV1E_HUMAN	P01600 homo sapien
8	35	100.0	108	KV5P_MOUSE	P01649 mus musculu
9	35	100.0	108	KV5Q_MOUSE	P01650 mus musculu
10	35	100.0	108	KV5R_MOUSE	P01651 mus musculu
11	35	100.0	108	KV5S_MOUSE	P01652 mus musculu
12	35	100.0	108	KV5T_MOUSE	P01653 mus musculu
13	35	100.0	109	KV01_RAT	P01681 rattus norv
14	35	100.0	109	KV1T_HUMAN	P01612 homo sapien
15	35	100.0	109	KV3B_HUMAN	P01620 homo sapien
16	35	100.0	109	KV3D_HUMAN	P01622 homo sapien
17	35	100.0	109	KV3E_HUMAN	P01623 homo sapien
18	35	100.0	109	KV3G_HUMAN	P04206 homo sapien
19	35	100.0	109	KV4D_HUMAN	P03593 homo sapien
20	35	100.0	111	KV3H_MOUSE	P01660 mus musculu
21	35	100.0	111	KV3J_MOUSE	P01662 mus musculu
22	35	100.0	111	KV3K_MOUSE	P01663 mus musculu
23	35	100.0	114	KV1A_MOUSE	P01632 mus musculu
24	35	100.0	114	KV4A_HUMAN	P01625 homo sapien
25	35	100.0	115	KV3I_HUMAN	P04433 homo sapien
26	35	100.0	115	KV5A_HUMAN	P06315 homo sapien
27	35	100.0	116	KV3J_HUMAN	P04434 homo sapien
28	35	100.0	117	KV1I_HUMAN	P01601 homo sapien
29	35	100.0	121	KV4D_HUMAN	P06312 homo sapien
30	35	100.0	129	KV1W_HUMAN	P04431 homo sapien
31	35	100.0	129	KV3L_HUMAN	P18135 homo sapien
32	35	100.0	129	KV3M_HUMAN	P18136 homo sapien
33	35	100.0	131	KV3I_MOUSE	P01661 mus musculu

34	35	100.0	133	1	KV4B_HUMAN	P06313 homo sapien
35	35	100.0	134	1	KV4C_HUMAN	P06314 homo sapien
36	35	100.0	136	1	KV5B_MOUSE	P01634 mus musculu
37	33	94.3	104	1	KV17_RABIT	P01698 cryptolagus
38	33	94.3	112	1	KV3G_MOUSE	P01659 mus musculu
39	33	94.3	132	1	KV3F_MOUSE	P01658 mus musculu
40	32	91.4	285	1	ALXM_PHOS4	P39049 photobacter
41	31	88.6	108	1	KV05_RABIT	P01686 cryptolagus
42	31	88.6	108	1	KV07_RABIT	P01688 cryptolagus
43	31	88.6	108	1	KV08_RABIT	P01689 cryptolagus
44	31	88.6	108	1	KV1A_HUMAN	P01593 homo sapien
45	31	88.6	108	1	KV1F_HUMAN	P01598 homo sapien

ALIGNMENTS

RESULT 1  
KV3C\_HUMAN STANDARD; PRT; 100 AA.  
AC P01621;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region NG9 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84093600; PubMed=6419127;  
RA Bentley D.L.;  
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to  
a small family of germ-line V genes.";  
RL Nature 307:77-80(1984).  
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.  
DR PIR; A01894; K3HUNG.  
DR HSSP; P80362; LWL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; Hybridoma.  
FT NON\_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.  
FT DISULFID 27 93 BY SIMILARITY.  
FT NON\_TER 100 100  
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;  
Query Match 100.0%; Score 35; DB 1; Length 100;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7  
Db 74 TDFTLTI 80

RESULT 2  
KV04\_RABIT STANDARD; PRT; 107 AA.  
AC P01685;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V region 4135.

OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cricetidae;  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75133568; PubMed=1091650;  
RA Chen K.C.S., Kindt T.J., Krause R.M.;  
RT "Primary structure of the L chain from a rabbit homogeneous antibody  
RT to streptococcal carbohydrate. II. Sequence determination of peptides  
RT from tryptic and peptic digests.";  
RJ J. Biol. Chem. 250:3289-3296(1975).  
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE R4-TYPE C REGION IS ALSO GIVEN.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE  
CC SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI AND WAS ISOLATED  
CC FROM THE SERUM OF A SINGLE RABBIT.  
DR PIR: A01949; K4RB41.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR Immunoglobulin V region.  
KW Immunoglobulin V region; Glycoprotein.  
FT CARBOHYD 28 N-LINKED (GLCNAC...)  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11182 MW; 8F84C5FEE60B7222 CRC64;  
Query Match 100.0%; Score 35; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : TDFTLTI 7  
Db 70 TDFTLTI 76  
RESULT 3  
KV1D HUMAN STANDARD; PRT; 107 AA.  
AC P01596;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75075135; PubMed=4216454;  
RA Milstein C.P., Deverson E.V.;  
RT "Primary structure of kappa light chain from a human myeloma  
RT protein.";  
RL Eur. J. Biochem. 49:377-382(1974).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
CC MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR: A01864; K1HUAR.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Glycoprotein.  
FT CARBOHYD 28 N-LINKED (GLCNAC...)  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; E1BF05F9844C3346 CRC64;  
Query Match 100.0%; Score 35; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TDFTLTI 7  
Db 69 TDFTLTI 75  
RESULT 4  
KV06 RABBIT STANDARD; PRT; 108 AA.  
AC P01687;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V region BS-5.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cricetidae;  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75127348; PubMed=4156171;  
RA Jaton J.-C.;  
RT "Comparison of the amino acid sequences of the variable regions of  
RT light chains derived from two homogeneous rabbit anti-pneumococcal  
RT antibodies.";  
RJ Biochem. J. 141:15-25(1974).  
RN [2]  
RP AMIDES AT POSITIONS 37 AND 69.  
RA Jaton J.-C.;  
RJ Submitted (JUN-1975) to the PIR data bank.  
CC -!- MISCELLANEOUS: THIS CHAIN DIFFERS FROM THE KAPPA CHAIN FROM RABBIT  
CC BS-1, ALSO OBTAINED FROM ANTIBODY TO TYPE II: PNEUMOCOCCI, AT 8  
CC POSITIONS IN THE V REGION.  
DR PIR: A90274; KVRBB5.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT DISULFID 80 >108  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11281 MW; CFB6C10DBB7A5FCE CRC64;  
Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TDFTLTI 7  
Db 69 TDFTLTI 75

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR; A01868; KIHUHU.  
DR HSSP; P80362; IWTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 98 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6163D8D0618 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 7  
KV1H HUMAN STANDARD; PRT; 108 AA.  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Scw.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of  
R: kappa-type (Bence-Jones protein Scw.); 11: The chymotryptic peptides  
R: and the complete amino acid sequence."  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR; A01875; KIHUSW.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 98 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BCD6E350017FLE51 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 6  
KV1H HUMAN STANDARD; PRT; 108 AA.  
AC P01600;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
chain of subgroup 1 (Bence-Jones Protein Hau); subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 5  
KV1E HUMAN STANDARD; PRT; 108 AA.  
AC P01597;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region DEE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstein C.P., Deverson E.V.;  
RT "The amino acid sequence of a human kappa light chain."  
RL Biochem. J. 123:945-958(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR; A01865; KIHUDE.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 98 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BCD6E350017FLE51 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 4  
KV1G HUMAN STANDARD; PRT; 108 AA.  
AC P01603;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
chain of subgroup 1 (Bence-Jones Protein Hau); subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 3  
KV1F HUMAN STANDARD; PRT; 108 AA.  
AC P01602;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
chain of subgroup 1 (Bence-Jones Protein Hau); subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 2  
KV1D HUMAN STANDARD; PRT; 108 AA.  
AC P01601;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
chain of subgroup 1 (Bence-Jones Protein Hau); subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75

RESULT 1  
KV1C HUMAN STANDARD; PRT; 108 AA.  
AC P01600;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
chain of subgroup 1 (Bence-Jones Protein Hau); subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

Query Match 100.0%; Score 35; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative C; Mismatches C; Indels C; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 69 TDFTLTI 75



```
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
AC P01653;
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11876 YW; 35C116BD60F79310 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 TDFTLTI 7
Db 69 TDFTLTI 75

RESULT 11
KVSS_MOUSE STANDARD; PRT; 108 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
DC Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; B92811; KVM582.
DR HSSP; P80362; LWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
AC P01652;
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 TDFTLTI 7
Db 69 TDFTLTI 75
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RESULT 12
KVST_MOUSE STANDARD; PRT; 108 AA.
AC P01653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; B92811; KVM582.
DR HSSP; P80362; LWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
AC P01653;
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
Db 69 TDFTLTI 75

RESULT 13
KVCL_RAT STANDARD; PRT; 109 AA.
AC P01681;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V region S211.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Louvain;
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
phylogenetic relationships of V- and C-region genes."
RL J. Immunol. 115:59-62(1975).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01944; KVRT21.
```



```
DR HSSP; P01607; IREL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 35 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 36 50 FRAMEWORK-2.
FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 58 89 FRAMEWORK-3.
FT DOMAIN 90 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108 FRAMEWORK-4.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11347 MW; A25BPF8F9FD5C84C6 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 70 TDFTLTI 76

RESULT 14
KVIT_HUMAN
ID KVIT_HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-J region Mav.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic
Bence-Jones Protein (Mav). An unusual insertion in the third
hypervariable region of a human kappa-immunoglobulin light chain.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
FOUND.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR; A01879; KIHUV.
DR HSSP; P80362; LWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108 FRAMEWORK-4.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11870 MW; B6ABF4515D55F5A0 CRC64;
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Query Match 100.0%; Score 35; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 15
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
group.";
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
DR HSSP; P80362; LWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7699C3ECD646FFB4 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 70 TDFTLTI 76

Search completed: October 4, 2003, 12:22:36
Job time : 10.6667 secs
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GenCore version 5.1.6  
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DM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:17:13 ; Search time 49.6667 Seconds  
(without alignments):  
36.370 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFLT 7

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%  
Maximum Match: 100%  
Listing first 45 summaries

Database : SPTRMBL23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	107	4 Q9UL81	Q9ul81 homo sapien
2	35	100.0	107	4 Q96SA9	Q96sa9 homo sapien
3	35	100.0	107	11 Q9ER29	Q9er29 mus musculu
4	35	100.0	108	4 Q9UL76	Q9ul76 homo sapien
5	35	100.0	108	4 Q9UL77	Q9ul77 homo sapien
6	35	100.0	108	4 Q9UL79	Q9ul79 homo sapien
7	35	100.0	108	11 Q8VIJ0	Q8vi10 mus musculu
8	35	100.0	109	4 Q9UL86	Q9ul86 homo sapien
9	35	100.0	109	4 Q9UL78	Q9ul78 homo sapien
10	32	91.4	109	6 Q9NOW5	Q9now5 cryptotlagus
11	32	91.4	557	16 Q99XR2	Q99xr2 streptococc
12	32	91.4	557	16 Q8NZ49	Q8nz49 streptococc
13	32	91.4	557	16 Q8K5J8	Q8ks18 streptococc
14	31	88.6	99	11 Q9UL74	Q9jl74 mus musculu
15	31	88.6	108	4 Q9UL83	Q9ul83 homo sapien
16	31	88.6	109	4 Q9UL85	Q9ul85 homo sapien

17	31	88.6	110	9 Q94MB9	Q94mb9 bacterioph
18	31	88.6	110	9 Q94LZ7	Q94lz7 bacterioph
19	31	88.6	110	9 Q94MG5	Q94mg5 bacterioph
20	31	88.6	110	9 Q94LY9	Q94ly9 bacterioph
21	31	88.6	110	9 Q94LZ6	Q94lz6 bacterioph
22	31	88.6	110	9 Q94MC3	Q94mc3 bacterioph
23	31	88.6	110	9 Q94MC2	Q94mc2 bacterioph
24	31	88.6	110	9 Q94MC1	Q94mc1 bacterioph
25	31	88.6	234	4 Q8NEK1	Q8nek1 homo sapien
26	31	88.6	264	16 Q8DFD5	Q8dfd5 vibrio vuln
27	31	88.6	313	4 Q8N303	Q8nh03 homo sapien
28	31	88.6	318	4 Q8NGX1	Q8ngx1 homo sapien
29	31	88.6	428	16 Q8ZFB5	Q8zfb5 yersinia pe
30	31	88.6	572	10 Q9AT27	Q9at27 phytoptchr
31	31	88.6	4199	16 P74440	P74440 synechocyst
32	30	85.7	110	9 Q94MG4	Q94mg4 bacterioph
33	30	85.7	111	11 Q920E9	Q920e9 mus musculu
34	30	85.7	229	2 Q9AJ88	Q9aj88 pseudomonas
35	30	85.7	276	8 Q02656	Q02656 podospora a
36	30	85.7	280	5 O17867	O17867 caenorhabdi
37	30	85.7	320	11 Q99LQ3	Q99lq3 mus musculu
38	30	85.7	408	2 Q8RU02	Q8ru02 methylobaci
39	30	85.7	412	5 O45223	O45223 caenorhabdi
40	30	85.7	415	5 Q9TZG2	Q9tzg2 caenorhabdi
41	30	85.7	416	16 Q8Y073	Q8y073 ralstonia s
42	30	85.7	497	4 Q9NV09	Q9rv09 homo sapien
43	30	85.7	553	4 Q8TDD5	Q8tdd5 homo sapien
44	30	85.7	553	11 Q8R4F0	Q8r4f0 mus musculu
45	30	85.7	591	11 Q8BSG1	Q8bsg1 mus musculu

ALIGNMENTS

RESULT 1  
Q9UL81  
ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
CS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID:9606;  
RN :1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -.  
DR HSSP; P01607; IREI  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
  
Query Match 100.0%; Score 35; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TDFLT 7  
|||||

Db 69 TDFTLTI 75

# RESULT 2

Q96SA9 PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal antibodies from  
 RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes."  
 RJ J. Immunol. 161:2020-2031(1998).  
 DR EMBL; U96396; AAB68785.1;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 107 107  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11520 MW; 48B43B9C5B577F16 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 69 TDFTLTI 75

# RESULT 3

Q9ERZ9 PRELIMINARY; PRT; 107 AA.  
 AC Q9ERZ9;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Anti human TNF-alpha light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
 RT "Cloning and sequencing of the light chain fragment of variable region  
 RT genes of an anti-hTNF-a monoclonal antibody."  
 RJ J. Cell. Mol. Immunol. 12:21-26(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
 RT "Construction and sequencing of the single-chain antibody gene of a  
 RT human TNF-alpha specific monoclonal antibody."  
 RJ Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
 RJ Submitted (MAY-2000) to the EMBL/GenBank/DBC databases.  
 DR EMBL; AF262753; AAG23804.1; -.

DR HSSP; P8C362; LWTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 107 107  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;  
 Query Match 100.0%; Score 35; DB 11; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TDFTLTI 7

Db 72 TDFTLTI 78

# RESULT 4

Q9UL70 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL70;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.J., Kalis M.N., Beiney S.N.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RJ Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035044; AAD56280.1; -.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11633 MW; BTBEDC3E41FCCA37 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 69 TDFTLTI 75

# RESULT 5

Q9UL77 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL77;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

QX NCBI\_TaxID=9606;  
RN [1]  
RRP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RRL Clin. Immunol. Immunopathol. 97:184-192(1998).  
RML EMBL; AF035037; AAD56271.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C0668175C4D16F3 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
Db |||||  
69 TDFTLTI 75

## RESULT 6

Q9UL79 PRELIMINARY; PRT; 108 AA.  
Q9UL79;  
AC 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RRP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RRL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RML EMBL; AF035035; AAD56271.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11787 MW; D55845F19724FB4E CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
Db |||||  
69 TDFTLTI 75

## RESULT 7

Q8VIJ0 PRELIMINARY; PRT; 108 AA.  
AC Q8VIJ0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-DNA light chain (Fragment).  
GN VK19.  
OS Mus musculus (Mouse).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RRP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HeJ-lpr/lpr;  
RX MEDLINE=96409289; PubMed=8814271;  
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gillespie G.S.;  
RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis";  
RL Eur. J. Immunol. 26:2225-2233(1996).  
DR EMBL; U59155; AAC02917.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 100.0%; Score 35; DB 11; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
Db |||||  
69 TDFTLTI 75

## RESULT 8

Q9UL86 PRELIMINARY; PRT; 109 AA.  
AC Q9UL86;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin kappa chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RRP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RRL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RML EMBL; AF035028; AAD56264.1; -.  
DR HSSP; P80362; IWTI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7D8AC83 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:||||  
Db 70 TDFTLTI 76

RESULT 9

Q9UL78 Q9UL78 PRELIMINARY; PRT; 109 AA.  
AC Q9UL78;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.Y., Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RT Clin. Immunol. Immunopathol. 87:194-192(1998).  
RL EMBL; AF035036; AAD56272.1; -;  
DR HSSP; P80362; 1WT.L.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52E075E197 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:||||  
Db 70 TDFTLTI 76

RESULT 10

Q9NOW5 Q9NOW5 PRELIMINARY; PRT; 109 AA.  
AC Q9NOW5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-human A33 light chain variable region (Fragment).  
DE Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20250927; PubMed=10788485;  
RA Rader C., Ritter G., Nathan S., Elia M., Gout I., Jungbluth A.A., Cohen L.S., Weit S., Old L.J., Barbas C.F. III;  
RA "The rabbit antibody repertoire as a novel source for the generation of therapeutic human antibodies";  
RT J. Biol. Chem. 275:13668-13676(2000).  
RL EMBL; AF245502; AAF68449.1; -;  
DR HSSP; P80362; 1WT.L.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11323 MW; BD8B396EE75F94FB CRC64;  
  
Query Match 91.4%; Score 32; DB 6; Length 109;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:||||  
Db 69 TDFTLTI 75

RESULT 11

Q99XR2 Q99XR2 PRELIMINARY; PRT; 557 AA.  
AC Q99XR2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative formate-tetrahydrofolate ligase (EC 6.3.4.3).  
GN FHS.2 OR SPY2085.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae;  
CC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=SF370 / ATCC 700294 / Serotype M1;  
RX MEDLINE=21192684; PubMed=11296296;  
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.C., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White C., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
DR EMBL; AE006628; AAK34738.1; -;  
DR InterPro; IPR000559; Fmtethyd\_synth.  
DR Pfam; PF01268; FTHFS; 1.  
DR PROSITE; PS00722; FTHFS\_2; 1.  
KW Ligase; Complete proteome.  
SQ SEQUENCE 557 AA; 59053 MW; CB07C9FCE90B34E7 CRC64;

Query Match 91.4%; Score 32; DB 16; Length 557;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:||||  
Db 505 TDFTLTI 511

RESULT 12

Q8NZ49 Q8NZ49 PRELIMINARY; PRT; 557 AA.  
AC Q8NZ49;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative formate-tetrahydrofolate ligase.  
GN SPYMI8\_2144.  
OS Streptococcus pyogenes (serotype M18).  
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae;  
CC Streptococcus.  
OX NCBI\_TaxID=186103;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=MGAS8232 / Serotype M18;  
RX MEDLINE=21927593; PubMed=11917128;  
RA Smoot J.C., Barbican K.D., Van Gompel J.C., Smoot J.M., Chaussee M.S.,  
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,  
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.N., Zhang Q.,  
RA Kapur V., Daly J.A., Veasy J.G., Musser J.M.;  
RT "Genome sequence and comparative microarray analysis of serotype M18  
RT group A Streptococcus strains associated with acute rheumatic fever  
RT outbreaks.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
DR EMBL: AE010116; AAL98933.1; --  
DR InterPro; IPR000559; Fmethyl\_synth.  
DR Pfam; PF01268; FTHFS.2;  
DR PROSITE; PS00722; FTHFS.2; 1.  
KW Ligase; Complete proteome; Hypothetical protein.  
SQ SEQUENCE 557 AA; 59054 MW; 7A7222A02BDSA804 CRC64;

Query Match 91.4%; Score 32; DB 16; Length 557;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:|  
Db 505 TDFTVTI 511

## RESULT 13

Q8K5L8 PRELIMINARY; PRT; 557 AA.  
AC Q8K5L8;  
DT 01-OCT-2002 (TREMBLrel. 22, Created);  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);  
DE Putative formate-tetrahydrofolate ligase.  
GN FHS.2 OR SPYM3 1776.  
OS Streptococcus pyogenes (serotype M3).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
DC Streptococcus.  
DX NCBI\_TaxID=198466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MGAS315 / Serotype M3;  
RX MEDLINE=22133803; PubMed=12122206;  
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,  
RA Marmarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,  
RA Campbell D.S., Smith T.N., McCormick J.K., Leung D.Y.X.,  
RA Schlievert P.M., Musser J.M.;  
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:  
RT phage-encoded toxins, the high-virulence phenotype, and clone  
RT emergence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).  
DR EMBL: AE014171; AAY80383.1; --  
DR InterPro; IPR000559; Fmethyl\_synth.  
DR Pfam; PF01268; FTHFS.2;  
DR PROSITE; PS00722; FTHFS.2; 1.  
KW Ligase; Complete proteome; Hypothetical protein.  
SQ SEQUENCE 557 AA; 59051 MW; 029820DF95BB401A CRC64;

Query Match 91.4%; Score 32; DB 16; Length 557;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:|  
Db 505 TDFTVTI 511

## RESULT 14

29JUL74 PRELIMINARY; PRT; 99 AA.  
AC 29JUL74;  
DT 01-OCT-2000 (TREMBLrel. 15, Created);  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);  
DE Anti-myosin immunoglobulin light chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin.";  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL: AF206032; AAF69333.1; --  
DR HSSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 99  
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 88.6%; Score 31; DB 11; Length 99;  
Best Local Similarity 85.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||:|  
Db 61 TDFTFTI 67

## RESULT 15

Q9JUL83 PRELIMINARY; PRT; 108 AA.  
AC Q9JUL83;  
DT 01-MAY-2000 (TREMBLrel. 13, Created);  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update);  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035031; AAD56267.1; --  
DR HSSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 88.6%; Score 31; DB 4; Length 108;  
Best Local Similarity 85.7%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFLT 7  
|:|:|:|  
Db 69 TDFLT 75

Search completed: October 4, 2003, 12:25:17  
Job time : 52.6667 secs

GenCore version 5.1.6  
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MM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:26 ; Search time 60.3333 Seconds  
(without alignments)  
18.416 Million cells updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFLLT? 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	35	100.0	16	AA41874	Rheumatoid arthritis
2	35	100.0	16	AAU25389	Schizophrenia-Asso
3	35	100.0	16	AAU15733	Schizophrenia-Asso
4	35	100.0	16	ABG78872	Multiple sclerosis
5	35	100.0	22	ABP56613	Kappa light chain
6	35	100.0	29	ABP62758	Human immunopeptid
7	35	100.0	32	AAH87043	Human group 1 light
8	35	100.0	32	AAU52745	Humanised ACP-5 L
9	35	100.0	32	AAH96286	Anti-A33 antigen

10	35	100.0	32	AAH96288	Anti-A33 antigen 1
11	35	100.0	32	AAH97666	A33 antigen bindin
12	35	100.0	32	AAH97668	A33 antigen bindin
13	35	100.0	32	ABG98287	Human antibody 012
14	35	100.0	32	ABP62656	Human immunopeptid
15	35	100.0	32	ABP62657	Human immunopeptid
16	35	100.0	32	ABP62658	Human immunopeptid
17	35	100.0	32	ABP62659	Human immunopeptid
18	35	100.0	32	ABP62660	Human immunopeptid
19	35	100.0	32	ABP62661	Human immunopeptid
20	35	100.0	32	ABP62664	Human immunopeptid
21	35	100.0	32	ABP62666	Human immunopeptid
22	35	100.0	32	ABP62667	Human immunopeptid
23	35	100.0	32	ABP62668	Human immunopeptid
24	35	100.0	32	ABP62669	Human immunopeptid
25	35	100.0	32	ABP62670	Human immunopeptid
26	35	100.0	32	ABP62671	Human immunopeptid
27	35	100.0	32	ABP62675	Human immunopeptid
28	35	100.0	32	ABP62676	Human immunopeptid
29	35	100.0	32	ABP62677	Human immunopeptid
30	35	100.0	32	ABP62678	Human immunopeptid
31	35	100.0	32	ABP62680	Human immunopeptid
32	35	100.0	32	ABP62682	Human immunopeptid
33	35	100.0	32	ABP62683	Human immunopeptid
34	35	100.0	32	ABP62684	Human immunopeptid
35	35	100.0	32	ABP62685	Human immunopeptid
36	35	100.0	32	ABP62687	Human immunopeptid
37	35	100.0	32	ABP62688	Human immunopeptid
38	35	100.0	32	ABP62689	Human immunopeptid
39	35	100.0	32	ABP62690	Human immunopeptid
40	35	100.0	32	AAO17642	Human PAPalpha spe
41	35	100.0	32	AAO17650	Human PAPalpha spe
42	35	100.0	32	AAE19672	Human group 1 cons
43	35	100.0	32	AAE19673	Human tumour necro
44	35	100.0	32	AAU70396	Human light chain
45	35	100.0	32	AAU70404	Human light chain

ALIGNMENTS

RESULT 1

AA41874  
ID AA41874 standard; Peptide; 16 AA.  
XX  
AC AA41874;  
XX  
DT 09-DEC-1999 (first entry)  
XX  
DE Rheumatoid arthritis diagnostic protein isoform peptide #25.  
XX  
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;  
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;  
KW rheumatoid arthritis diagnostic protein isoform; screening;  
KW expression reference protein isoform; prognosis.  
XX  
OS Homo sapiens.  
XX  
PK WC9947925-A2.  
XX  
PF 23-SEP-1999.  
XX  
RF 15-MAR-1999; 99WO-GB00763.  
XX  
RR 13-MAR-1996; 96GB-0005477.  
XX  
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
XX  
PI Parekh RB, Patel TP, Townsend RR;  
XX  
DR WPZ; 1999-571871/48.  
XX  
PT Diagnosis of human rheumatoid arthritis by two-dimensional



PT electrophoresis -

PS Disclosure; Page 18; 157pp; English.

XX  
XX  
XX  
CC A method has been developed for the diagnosis of human rheumatoid  
CC arthritis (RA) using two-dimensional electrophoresis to generate a  
CC two-dimensional array of features. The method can be used for screening,  
CC diagnosis and prognosis of RA in a subject or for monitoring the effect  
CC of an anti-RA drug or therapy administered to a subject. The method  
CC comprises: (a) analysing a sample of serum or plasma and optionally  
CC synovial fluid by two-dimensional electrophoresis, to generate a two-  
CC dimensional array of features; (b) identifying at least one chosen  
CC feature whose relative abundance correlates with the presence or absence  
CC of RA; and (c) comparing the abundance of each chosen feature in the  
CC sample with the abundance of that chosen feature in serum or plasma from  
CC one or more persons without RA, where the relative abundance of the  
CC chosen feature or features in the sample indicates the presence or  
CC absence of RA in the subject. The method can also be used in clinical  
CC studies for testing drugs for therapy of RA, for purification of RA-  
CC diagnostic protein isoforms (RPIs), and for production of antibodies to  
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify  
CC compounds that promote or inhibit their activity, which are then used as  
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy  
CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to  
CC AAY42103 represent expression reference protein isoform peptides and  
CC AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all  
CC used in the exemplification of the present invention.

XX Sequence 16 AA;

Query Match: 100.0%; Score 35; DB 20; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
| | | | |  
DB 8 TDFTLTI 14

RESULT 2

AAU25389  
ID AAU25389 standard; Peptide; 16 AA.

XX AC AAU25389;

XX 18-DEC-2001 (first entry)

XX Schizophrenia-Associated Protein Isoform (SPI) peptide #618.

XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX Homo sapiens.

XX WO200162785-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB30792.

XX 24-FEB-2000; 2000GB-0004415.

XX 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570624/64.

XX New schizophrenia associated protein isoforms and encoding nucleic acid  
PT molecules, useful for treatment, diagnosis and prognosis of  
PT schizophrenia and screening for potential drugs for treatment and new  
PT drug targets -

XX  
PS Disclosure; Page 41; 148pp; English.

XX  
XX  
CC The sequence represents a schizophrenia-associated protein isoform (SPI).  
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
CC in cerebrospinal fluid, serum or plasma and are useful markers of  
CC schizophrenia. The sequences can be used for treatment and diagnosis of  
CC schizophrenia. Screening, prognosis, monitoring the results of therapy,  
CC identifying patients most likely to respond to a particular therapy and  
CC identification of new targets for drug treatment. SPI DNA is useful as a  
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX Sequence 16 AA;

Query Match: 100.0%; Score 35; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
| | | | |  
DB 8 TDFTLTI 14

RESULT 3

AAU15733

ID AAU15733 standard; Peptide; 16 AA.

XX AC AAU15733;

XX 24-OCT-2001 (first entry)

XX Schizophrenia-associated isoform peptide #618.

XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
KW neurological disorder; neuropathy.

XX Homo sapiens.

XX WO200163293-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00783.

XX 24-FEB-2000; 2000GB-0004415.

XX 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMCAC, Parekh RB, Rohlf C;

XX WPI; 2001-502868/55.

XX Diagnosing and monitoring Schizophrenia by detecting the presence of  
PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
PT Isoforms in samples of cerebrospinal fluid -

XX Claim 6; Page 41; 160pp; English.

XX The invention relates to methods and compositions for screening,  
CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH  
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,  
CC studying the effectiveness of treatments and for identifying potential  
CC therapeutic agents. The method is used for (1) screening or diagnosis of  
CC SCH and the relative abundance of at least 1 chosen feature correlates  
CC with the presence or absence of SCH; and (2) monitoring the effect of  
CC therapy administered to a subject with SCH and the relative abundance of  
CC at least 1 chosen feature which correlates with the severity of SCH.  
CC The expression and activity of the SFS, SPIs and related molecules  
CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
CC progress of the disorder and the effectiveness of treatment and as

CC targets to identify and produce potential therapeutic agents for the  
CC treatment of SCH. The paucity of detectable neurologic defects  
CC distinguishes neuropsychiatric disorders such as SCH from neurological  
CC disorders, where manifestations of anatomical and biochemical changes  
CC have been identified in many cases. Consequently the identification and  
CC characterisation of cellular and/or molecular causative defects and  
CC neuropathies are necessary for improved treatment of neuropsychiatric  
CC disorders. AAU15:14-AAU15762 represent the amino acid sequences of  
CC schizophrenia-associated isoforms used in the method of the invention.  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 35; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 TDFTLTI 7  
|||  
Db 8 TDFTLTI 14

RESULT 4  
ABG78872  
D ABG78872 standard; Peptide; 16 AA.

AC ABG78872;  
XX 29-NOV-2002 (first entry)

XX Multiple sclerosis associated feature (MSF) tryptic digest peptide #360.  
XX Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;  
XX human; multiple sclerosis-associated protein isoform; MSPI;  
XX antiinflammatory; neuroprotective.

XX Homo sapiens.  
XX WO200259604-A2.  
XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-GB03330.  
XX 26-JAN-2001; 2001US-264404P.  
XX 20-NOV-2001; 2001US-331647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX Herath HMCAC, Perakk RB, Rohiff C;  
XX WPI; 2002-593812/64.

XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.  
XX determining the stage or severity of MS, comprises detecting the  
XX presence of MS-associated features or protein isoforms by 2-dimensional  
XX electrophoresis.

XX Disclosure; Page 36; 128pp; English.

XX This invention relates to a novel method for screening or diagnosing  
XX multiple sclerosis (MS) in a subject to determine the stage or severity  
XX of MS, to identify a subject at risk of developing MS or to monitor the  
XX effect of a therapy administered. The method comprises analysing a  
XX sample body fluid from the subject by two-dimensional electrophoresis  
XX and detecting the presence of multiple sclerosis-associated features  
XX (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).  
XX The MSFs of the invention correspond to spots identified on a 2D gel  
XX these proteins may have antiinflammatory or neuroprotective activity.  
XX The methods of the invention and the compositions are useful for  
XX clinical screening, diagnosis and treatment of MS, for monitoring the  
XX effectiveness of MS treatment, for selecting participants in clinical  
XX trials, for identifying patients most likely to respond to a particular  
XX therapeutic treatment and for screening and developing drugs for

CC treatment of MS. Agents that modulate the expression or activity of an  
CC MSPI are useful for treating MS, for preventing or delaying the onset or  
CC development of MS, to prevent or delay the progression of MS, or to  
CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding  
CC an MSPI, MSPI-related polypeptide, or their fragments are useful for  
CC promoting MSPI function by gene therapy. The present sequence represents  
CC a human multiple sclerosis associated feature tryptic digest  
XX peptide of the invention.

SQ Sequence 16 AA;

Query Match 100.0%; Score 35; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||  
Db 8 TDFTLTI 14

RESULT 5  
ABP56813  
ID ABP56813 standard; Protein; 22 AA.

XX ABP56813;

XX 01-APR-2003 (first entry)

XX Kappa light chain A27:JH1 amino acid sequence #3.

XX Focused library; genetic package; antibody; kappa light chain; CDR;  
XX lambda light chain; heavy chain; complementary determining region;  
XX diversity.

XX Homo sapiens.  
XX Synthetic.

XX WO200261071-A2.

XX 08-AUG-2002.

XX 18-DEC-2001; 2001WO-US50297.

XX 18-DEC-2000; 2000US-256380P.

XX (LADN/) LADNER R C.

XX Ladner RC;

XX WPI; 2003-067343/06.

XX Focused library of vectors or genetic packages for displaying or  
XX expressing diversity of an antibody family, comprise variegated DNA  
XX sequences encoding heavy, kappa or lambda light chain complementary  
XX determining regions.

XX Disclosure; Page 68-69; 92pp; English.

XX The present invention describes a focused library of vectors or genetic  
XX packages that display, display and express, or comprise a member of a  
XX diverse family of human antibody related peptides, polypeptides and  
XX proteins and collectively display, display or express, or comprise a  
XX portion of the diversity of the antibody family, the vectors or genetic  
XX packages being characterised by variegated DNA sequences that encode a  
XX heavy chain, kappa or lambda light chain complementary determining region  
XX 1 (CDR1), CDR2 or CDR3. The focused library of vectors or genetic  
XX packages of the present invention are useful for displaying, or  
XX displaying and expressing the focused diversity of the family. The  
XX present invention, as compared to prior art, is less time consuming,  
XX more efficient and less cumbersome in the construction of libraries of  
XX vectors and genetic packages using diverse but focused populations of  
XX DNA sequences. ABP56771 to ABP56816 and ABZ22680 to ABZ22747 represent  
XX sequences used in the exemplification of the present invention.

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XX SQ Sequence 22 AA;
Query Match 100.0%; Score 35; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
Db 14 TDFTLTI 20

RESULT 6
ABP62758
ID ABP62758 standard; Peptide; 29 AA.
XX
AC ABP62758;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV NS 3 framework sequence #226.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW constructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
FN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US02303.
XX
PR 26-JAN-2001; 2001US-264451P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox R;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain
PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
PT (HCV), for diagnosing or treating patients having or suspected of
PT having HCV infection.
XX
PS Claim 4; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection.
XX
SQ Sequence 29 AA;
Query Match 100.0%; Score 35; DB 23; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
Db 13 TDFTLTI 19

RESULT 7
AAR87043
ID AAR87043 standard; Peptide; 32 AA.

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```

XX AAR87043;
AC
XX
DT 25-JUN-1996 (first entry)
XX
DE Human group I light chain framework 3.
XX
KW Humanised antibody; interleukin-5; IL-5; recombinant antibody;
KW antibody engineering; monoclonal antibody; VAB; 39D10; CDR;
KW complementarity determining region; light chain; framework;
KW eosinophilia; allergy; asthma.
XX
OS Homo sapiens.
XX
FN WO9535375-A1.
XX
PD 28-DEC-1995.
XX
PF 16-JUN-1995; 95WO-GB01411.
XX
PR 17-JUN-1994; 94GB-001223C.
XX
PA (CELLT ) CELLTECH THERAPEUTICS LTD.
XX
PI Achwal DS, Bodmer MW, Emtage JS;
XX
DR WPI; 1996-058412/06.
XX
PT Anti-human IL-5 recombinant antibody - useful for preventing or
PT reducing eosinophilia and for treating certain allergic diseases,
PT esp. asthma
XX
PS Example 3; Fig 3; 69pp; English.
XX
CC Framework regions (AAR87041-44) of human group I (gp1) germ line
CC antibody light chain showed homology to corresponding regions
CC (AAR87045-48, respectively) of the rat anti-human interleukin-5
CC monoclonal antibody 39D10 light chain (see AAR87040). This homology
CC was utilised in the prodr. of a humanised 39D10 VL (AAR87057) in
CC which rat 39D10 VL complementarity determining regions were grafted
CC into the human gp1 framework.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 35; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
Db 13 TDFTLTI 19

RESULT 8
AAY52745
ID AAY52745 standard; Peptide; 32 AA.
XX
AC AAY52745;
XX
DT 26-JAN-2000 (first entry)
XX
DE Humanised ATR-5 L chain V region FR3 for a.
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9951743-A1.
XX
PD 14-OCT-1999.

```

XX 02-APR-1999; 99WO-CP01768.  
XX 03-APR-1998; 98JP-0091850.  
XX (CHUS) CHUGAI SEIYAKU KK.  
XX Sato K, Adachi H, Yabuta N;  
XX WPI; 1999-620204/53.  
XX Humanised antibody recognizing human tissue factor, used for treatment  
XX of disseminated intravascular coagulation -  
XX Claim 17; Page 270; 281pp; Japanese.  
XX The present invention describes chimeric antibody (Ab) heavy (H) chains  
XX containing the variable region of the H chain of a mouse monoclonal Ab  
XX recognising human tissue factor (hTF) and the constant region of the H  
XX chain of a human Ab. The variable region is one of six specified  
XX sequences (which are the H chain variable regions from mouse monoclonal  
XX Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)  
XX chains containing the variable region of the L chain of a mouse  
XX monoclonal Ab recognising human tissue factor (hTF) and the constant  
XX region of the L chain of a human Ab, the variable region being one of six  
XX specified sequences (which are the L chain variable regions from mouse  
XX monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for  
XX the treatment and prevention of thrombotic disease, especially of  
XX disseminated intravascular coagulation (DIC). The humanised antibody has  
XX the high hTF binding activity of the mouse monoclonal antibody but  
XX greatly reduced immunogenicity. AA233051 to AA233091 and Y527007 to  
XX AAY52767 represent sequences used in the exemplification of the present  
XX invention.  
XX Sequence 32 AA;  
Q Query Match 100.0%; Score 35; DB 20; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 TDFTLTJI 7  
b 13 TDFTLTJI 19  
RESULT 9  
AAB98286  
D AAB98286 standard; Peptide; 32 AA.  
X AAB98286;  
X 20-AUG-2001 (first entry);  
X Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.  
X Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
X immunoglobulin; complementarity determining region; CDR; cancer;  
X cytostatic; anticancer; colon cancer; stomach cancer.  
X Homo sapiens.  
X WO200130393-A2.  
X 03-MAY-2001.  
X 20-OCT-2000; 2000WO-US29289.  
X 22-OCT-1999; 99US-0425638.  
X 04-APR-2000; 2000US-0543004.  
X (LUDW-) LUDWIG INST CANCER RES.  
X (SLOK) SLOAN KETTERING INST CANCER RES.  
X (SCRI) SCRIPPS RES INST.

XX Barbas CF, Ritter G, Welt S, Old LJ;  
XX WPI; 2001-328613/34.  
XX Treating cancers, particularly of stomach and colon, that express A33  
XX antigen by administering conjugate of anticancer agent with specific  
XX immunoglobulin product -  
XX Claim 16; Page 40; 85pp; English.  
XX The present invention describes a method for treating cancers that  
XX express the A33 antigen. The method comprises administering an  
XX anticancer agent (2) conjugated to an immunoglobulin product (1) that  
XX binds specifically to A33 and contains one or more of 13 specified  
XX complementarity determining regions (CDRs), given in AAB98286 to  
XX AAB98274. (1) has cytostatic activity. The method can be used for  
XX treating colon and stomach cancers. (11), or the nucleic acid encoding  
XX it, can be used directly, in unconjugated form, for immunotherapy of  
XX cancer, and, when labeled, for detection or diagnosis of diseases  
XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
XX AAB98321 represent sequences used in the exemplification of the  
XX present invention.  
XX Sequence 32 AA;  
Q Query Match 100.0%; Score 35; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TDFTLTJI 7  
Db 13 TDFTLTJI 19  
RESULT 10  
AAB98288  
ID AAB98288 standard; Peptide; 32 AA.  
XX AAB98288;  
AC AAB98288;  
XX 20-AUG-2001 (first entry)  
XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.  
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
XX immunoglobulin; complementarity determining region; CDR; cancer;  
XX cytostatic; anticancer; colon cancer; stomach cancer.  
XX Homo sapiens.  
XX WO200130393-A2.  
XX 03-MAY-2001.  
XX 20-OCT-2000; 2000WO-US29289.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543004.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX (SLOK) SLOAN KETTERING INST CANCER RES.  
XX (SCRI) SCRIPPS RES INST.  
XX Barbas CF, Ritter G, Welt S, Old LJ;  
XX WPI; 2001-328613/34.  
XX Treating cancers, particularly of stomach and colon, that express A33  
XX antigen by administering conjugate of anticancer agent with specific  
XX immunoglobulin product -  
XX Claim 16; Page 40; 85pp; English.

XX The present invention describes a method for treating cancers that  
CC express the A33 antigen. The method comprises administering an  
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that  
CC binds specifically to A33 and contains one or more of 13 specified  
CC complementarity determining regions (CDRs), given in AAB98262 to  
CC AAB98274. (I) has cytostatic activity. The method can be used for  
CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
CC it, can be used directly, in unconjugated form, for immunotherapy of  
CC cancer, and, when labeled, for detection or diagnosis of diseases  
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
CC AAB98321 represent sequences used in the exemplification of the  
CC present invention.  
XX  
XX Sequence 32 AA;  
SQ  
Query Match 100.0%; Score 35; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TDFTLTI 7  
Db 13 TDFTLTI 19  
RESULT 11  
AAB97666  
ID AAB97666 standard; Peptide; 32 AA.  
XX  
XX AAB97666;  
AC  
XX C8-AUG-2001 (first entry)  
DT  
XX A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.  
DE  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody; immunoglobulin.  
QW  
XX Homo sapiens.  
OS  
XX WO200131065-A1.  
PN  
XX  
XX 03-MAY-2001.  
PD  
XX 20-OCT-2000; 2000WO-US29026.  
PF  
XX 22-OCT-1999; 99US-3425638.  
PR  
XX C4-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing  
PT libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 9; Page 39; 62pp; English.  
PS  
XX The present invention describes a method for preparing a humanised rabbit  
CC antibody that specifically immunoreacts with a particular antigen. The  
CC method comprises expressing a library of antibodies comprising one or  
CC more complementarity determining region (CDR) from the variable domain  
CC sequences that specifically immunoreact with the antigen grafted into  
CC framework regions from humans, and selecting the antibodies that react  
CC with the antigen. The method is useful for humanising non-human  
CC mammalian antibodies, which can be used for the treatment of a variety  
CC of diseases. The present sequence represents an A33 antigen binding  
CC immunoglobulin product VLFR3 peptide which is given in an example from  
CC the present invention.  
XX  
XX

SQ Sequence 32 AA;  
Query Match 100.0%; Score 35; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TDFTLTI 7  
Db 13 TDFTLTI 19  
RESULT 12  
AAB97668  
ID AAB97668 standard; Peptide; 32 AA.  
XX  
XX AAB97668;  
AC  
XX 08-AUG-2001 (first entry)  
DT  
XX A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.  
DE  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody; immunoglobulin.  
QW  
XX Homo sapiens.  
OS  
XX WO200131065-A1.  
PN  
XX  
XX C3-MAY-2001.  
PD  
XX 20-OCT-2000; 2000WO-US29026.  
PF  
XX 22-OCT-1999; 99US-3425638.  
PR  
XX C4-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing  
PT libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 9; Page 39; 62pp; English.  
PS  
XX The present invention describes a method for preparing a humanised rabbit  
CC antibody that specifically immunoreacts with a particular antigen. The  
CC method comprises expressing a library of antibodies comprising one or  
CC more complementarity determining region (CDR) from the variable domain  
CC sequences that specifically immunoreact with the antigen grafted into  
CC framework regions from humans, and selecting the antibodies that react  
CC with the antigen. The method is useful for humanising non-human  
CC mammalian antibodies, which can be used for the treatment of a variety  
CC of diseases. The present sequence represents an A33 antigen binding  
CC immunoglobulin product VLFR3 peptide which is given in an example from  
CC the present invention.  
XX  
XX Sequence 32 AA;  
Query Match 100.0%; Score 35; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TDFTLTI 7  
Db 13 TDFTLTI 19  
RESULT 13  
ABG98287  
ID ABG98287 standard; Peptide; 32 AA.  
XX

XX AC ABG98287;  
XX AC  
XX DT 08-JAN-2003 (first entry)  
XX DT  
XX DE Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.  
XX DE  
XX AC Antibody; variable region; light chain; heavy chain; VH; VL; gp39;  
XX CD40; T-cell activation; B-cell differentiation; framework region;  
XX cellular immune response; gene therapy; graft rejection; human; FR;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;  
XX asthma; multiple sclerosis; allergy; diabetes mellitus;  
XX systemic lupus erythematosus; graft-versus-host disease.  
XX DT  
XX OS Homo sapiens.  
XX DE WO200194586-A2.  
XX PN  
XX DT 13-DEC-2001.  
XX DT  
XX PF 06-JUN-2001; 2001WO-US18098.  
XX AC  
XX PR 06-JUN-2000; 2000US-209584P.  
XX DT  
XX PA (IDEC-); IDEC PHARM CORP.  
XX DT  
XX PI Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;  
XX DT  
XX WI WIPI; 2002-188261/24.  
XX DT  
XX AC New antibodies binding to an epitope on gp39, useful for preventing  
XX graft rejection, or for treating autoimmune diseases (e.g. diabetes,  
XX asthma or multiple sclerosis), and non-autoimmune diseases (e.g.  
XX graft-versus-host disease)  
XX DT  
XX S Disclosure: Page 46; 130pp; English.  
XX DT  
XX C The invention relates to an antibody which binds to an epitope on gp39,  
XX is new, where the epitope is distinct from the epitope bound by IDEC-131,  
XX and the antibody has a non-agonistic effect on T-cell activation and  
XX inhibits gp39/CD40 interaction. Also included are: (1) an improved method  
XX of treating a disease by modulating gp39 expression or inhibiting the  
XX gp39/CD40 interaction comprising administering an antibody specific for  
XX gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of  
XX T-cell activation; (2) an antibody which antagonises B-cell  
XX differentiation and antibody production, and is non-agonistic of T-cell  
XX activation; (3) a DNA sequence which encodes an antibody defined above;  
XX (4) an expression vector, which contains a DNA sequence of (3);  
XX (5) a method of suppressing humoral and/or cellular immune responses  
XX against cells or vectors administered during cell or gene therapy  
XX comprising further administering prior, during or after gene therapy,  
XX an antibody defined above; and (6) an improved method of treatment which  
XX involves the transplantation of cells, tissues or organs of the same or  
XX different species into a subject, where the improvement comprises  
XX administering an antibody defined above prior, during or after  
XX transplantation, to suppress immune responses against the transplanted  
XX cell, tissue or organ, or to suppress immune responses elicited by the  
XX transplanted cell, tissue or organ against the host. The antibody is  
XX useful for preventing graft rejection, and for treating autoimmune  
XX diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes,  
XX asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or  
XX systemic lupus erythematosus, as well as non-autoimmune diseases such as  
XX graft-versus-host disease (many other diseases and conditions are  
XX given in the specification). The antibodies are also useful in gene or  
XX cellular therapy, and to inhibit humoral and cellular immune responses  
XX against viral vectors. The present sequence is a framework region  
XX (FR) fragment of a human anti-gp39 antibody used to determine which  
XX amino acids should be humanised in a mouse anti-gp39 molecule.  
XX Q  
XX Sequence 32 AA;

XX DT  
XX AC ABG98287;  
XX DT  
XX DE Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.  
XX DE  
XX AC Antibody; variable region; light chain; heavy chain; VH; VL; gp39;  
XX CD40; T-cell activation; B-cell differentiation; framework region;  
XX cellular immune response; gene therapy; graft rejection; human; FR;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;  
XX asthma; multiple sclerosis; allergy; diabetes mellitus;  
XX systemic lupus erythematosus; graft-versus-host disease.  
XX DT  
XX OS Homo sapiens.  
XX DE WO200194586-A2.  
XX PN  
XX DT 13-DEC-2001.  
XX DT  
XX PF 06-JUN-2001; 2001WO-US18098.  
XX AC  
XX PR 06-JUN-2000; 2000US-209584P.  
XX DT  
XX PA (IDEC-); IDEC PHARM CORP.  
XX DT  
XX PI Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;  
XX DT  
XX WI WIPI; 2002-188261/24.  
XX DT  
XX C The invention relates to an antibody which binds to an epitope on gp39,  
XX is new, where the epitope is distinct from the epitope bound by IDEC-131,  
XX and the antibody has a non-agonistic effect on T-cell activation and  
XX inhibits gp39/CD40 interaction. Also included are: (1) an improved method  
XX of treating a disease by modulating gp39 expression or inhibiting the  
XX gp39/CD40 interaction comprising administering an antibody specific for  
XX gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of  
XX T-cell activation; (2) an antibody which antagonises B-cell  
XX differentiation and antibody production, and is non-agonistic of T-cell  
XX activation; (3) a DNA sequence which encodes an antibody defined above;  
XX (4) an expression vector, which contains a DNA sequence of (3);  
XX (5) a method of suppressing humoral and/or cellular immune responses  
XX against cells or vectors administered during cell or gene therapy  
XX comprising further administering prior, during or after gene therapy,  
XX an antibody defined above; and (6) an improved method of treatment which  
XX involves the transplantation of cells, tissues or organs of the same or  
XX different species into a subject, where the improvement comprises  
XX administering an antibody defined above prior, during or after  
XX transplantation, to suppress immune responses against the transplanted  
XX cell, tissue or organ, or to suppress immune responses elicited by the  
XX transplanted cell, tissue or organ against the host. The antibody is  
XX useful for preventing graft rejection, and for treating autoimmune  
XX diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes,  
XX asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or  
XX systemic lupus erythematosus, as well as non-autoimmune diseases such as  
XX graft-versus-host disease (many other diseases and conditions are  
XX given in the specification). The antibodies are also useful in gene or  
XX cellular therapy, and to inhibit humoral and cellular immune responses  
XX against viral vectors. The present sequence is a framework region  
XX (FR) fragment of a human anti-gp39 antibody used to determine which  
XX amino acids should be humanised in a mouse anti-gp39 molecule.  
XX Q  
XX Sequence 32 AA;

Query Match: 100.0%; Score 35; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
DB 13 TDFTLTI 19

RESULT 14  
ABP62656  
ID ABP62656 standard; Peptide; 32 AA.  
XX  
AC ABP62656;  
XX  
DT 10-OCT-2002 (first entry)  
XX  
DE Human immunopeptide to HCV E2 glycoprotein framework sequence #164.  
XX  
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.  
XX  
OS Homo sapiens.  
XX PN WO200259340-A1.  
XX DT 01-AUG-2002.  
XX PF 25-JAN-2002; 2002WO-US02303.  
XX PR 26-JAN-2001; 2001US-264451P.  
XX PA (SCRI ) SCRIPPS RES INST.  
XX PI Maruyama T, Jones IM, Burton DR, Fox RI;  
XX WI WIPI; 2002-599801/64.  
XX DT  
XX PT New human immunopolypeptide with binding specificity for certain  
XX envelope glycoproteins and nonstructural proteins of hepatitis C virus  
XX (HCV), for diagnosing or treating patients having or suspected of  
XX having HCV infection  
XX  
PS Claim 4; Fig 17; 308pp; English.  
XX  
CC The present invention relates to human immunopolypeptides, produced by a  
XX phage transfection cell library. The present sequence is one such  
XX immunopolypeptide. The immunopolypeptides have binding specificity for  
XX envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
XX virus (HCV). E2 glycoprotein is believed to be responsible for target  
XX cell binding and contains neutralising epitopes, while NS3 is thought to  
XX be involved in the replication of HCV. The immunopolypeptides are useful  
XX for diagnosing and treating a patient having or suspected to be having  
XX HCV infection.  
XX  
SQ Sequence 32 AA;

Query Match: 100.0%; Score 35; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
DB 13 TDFTLTI 19

RESULT 15  
ABP62657  
ID ABP62657 standard; Peptide; 32 AA.  
XX  
AC ABP62657;  
XX  
DT 10-OCT-2002 (first entry)  
XX

DE Human immunopeptide to HCV E2 glycoprotein framework sequence #165.  
XX  
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
XX nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200259340-A1.  
XX  
PD C1-AUG-2002.  
XX  
PF 25-JAN-2002; 2002WO-US02303.  
XX  
PR 26-JAN-2001; 2001US-264451P.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Maruyama T, Jones IM, Burton DR, Fox RI;  
XX WPI; 2002-599801/64.  
XX  
PT New human immunopolypeptide with binding specificity for certain  
PT envelope glycoproteins and nonstructural proteins of hepatitis C virus  
PT (HCV), for diagnosing or treating patients having or suspected of  
PT having HCV infection -  
XX  
PS Claim 4; Fig 17; 308pp; English.  
XX  
CC The present invention relates to human immunopolypeptides, produced by a  
CC phage transfected cell library. The present sequence is one such  
CC immunopolypeptide. The immunopolypeptides have binding specificity for  
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
CC cell binding and contains neutralising epitopes, while NS3 is thought to  
CC be involved in the replication of HCV. The immunopolypeptides are useful  
CC for diagnosing and treating a patient having or suspected to be having  
CC HCV infection.  
XX  
SQ Sequence 32 AA;

Query Match 100.0%; Score 35; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLT 7  
| | | | |  
Db 13 TDFLT 19

Search completed: October 4, 2003, 12:21:57  
Job time : 60.3333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2003, 12:25:27 ; Search time 35.3333 Seconds  
Without alignments:  
31.344 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFLTIT 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	35	100.0	16	10	US-09-791-378-618 Sequence 618, Appl
2	35	100.0	32	9	US-09-855-271-13 Sequence 13, Appl
3	35	100.0	32	10	US-09-828-708-95 Sequence 95, Appl
4	35	100.0	32	10	US-09-828-708-97 Sequence 97, Appl
5	35	100.0	32	10	US-09-828-708-98 Sequence 98, Appl
6	35	100.0	32	10	US-09-828-708-100 Sequence 100, Appl
7	35	100.0	32	10	US-09-828-708-101 Sequence 101, Appl
8	35	100.0	32	10	US-09-949-559-91 Sequence 91, Appl
9	35	100.0	32	10	US-09-949-559-92 Sequence 92, Appl
10	35	100.0	32	11	US-09-874-141-15 Sequence 15, Appl
11	35	100.0	32	11	US-09-875-221A-91 Sequence 91, Appl
12	35	100.0	32	11	US-09-875-221A-92 Sequence 92, Appl
13	35	100.0	32	11	US-09-563-222-76 Sequence 76, Appl
14	35	100.0	32	11	US-09-563-222-84 Sequence 84, Appl
15	35	100.0	32	11	US-09-563-222-88 Sequence 88, Appl

16	35	100.0	32	11	US-09-563-222-116 Sequence 116, App
17	35	100.0	32	12	US-10-160-506-15 Sequence 15, Appl
18	35	100.0	32	12	US-10-160-506-112 Sequence 112, App
19	35	100.0	32	22	US-10-160-506-122 Sequence 122, App
20	35	100.0	36	12	US-10-327-645-5 Sequence 5, Appl
21	35	100.0	42	11	US-09-874-141-17 Sequence 17, Appl
22	35	100.0	42	11	US-09-874-141-18 Sequence 18, Appl
23	35	100.0	42	11	US-09-874-141-22 Sequence 22, Appl
24	35	100.0	42	11	US-09-874-141-23 Sequence 23, Appl
25	35	100.0	42	11	US-09-874-141-24 Sequence 24, Appl
26	35	100.0	70	12	US-10-171-681-9 Sequence 9, Appl
27	35	100.0	70	12	US-10-171-681-9 Sequence 9, Appl
28	35	100.0	73	15	US-10-078-938-13 Sequence 13, Appl
29	35	100.0	74	14	US-10-025-687-23 Sequence 23, Appl
30	35	100.0	74	15	US-10-125-687-23 Sequence 23, Appl
31	35	100.0	76	13	US-09-187-673-37 Sequence 37, Appl
32	35	100.0	79	12	US-10-171-681-14 Sequence 14, Appl
33	35	100.0	79	12	US-10-171-680-14 Sequence 14, Appl
34	35	100.0	80	11	US-09-269-921-130 Sequence 130, App
35	35	100.0	80	11	US-09-509-098-131 Sequence 131, App
36	35	100.0	80	12	US-10-160-506-8 Sequence 8, Appl
37	35	100.0	80	12	US-10-160-506-13 Sequence 13, Appl
38	35	100.0	80	12	US-10-160-506-114 Sequence 114, App
39	35	100.0	80	12	US-10-160-506-124 Sequence 124, App
40	35	100.0	80	12	US-10-171-681-12 Sequence 12, Appl
41	35	100.0	80	12	US-10-171-681-13 Sequence 13, Appl
42	35	100.0	80	12	US-10-171-681-15 Sequence 15, Appl
43	35	100.0	80	12	US-10-171-680-12 Sequence 12, Appl
44	35	100.0	80	12	US-10-171-680-13 Sequence 13, Appl
45	35	100.0	80	12	US-10-171-680-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-791-378-618  
; Sequence 618, Application US/09791378  
; Patent No. US20020142303A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; FILE REFERENCE: 9195-061-999  
; CURRENT APPLICATION NUMBER: US/09/791,378  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 618  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-378-618

Query Match 100.0%; Score 35; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTIT 7  
|||||  
DB 8 TDFLTIT 14

RESULT 2  
US-09-855-271-13  
; Sequence 13, Application US/09855271  
; Patent No. US20020042089A1  
; GENERAL INFORMATION:  
; APPLICANT: Bodmer, Mark W  
; APPLICANT: Achwal, Diljeet Singh  
; APPLICANT: Emtage, John Spencer



; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies

; FILE REFERENCE: CARP-0085

; CURRENT APPLICATION NUMBER: US/09/855,271

; CURRENT FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 09/347,061

; PRIOR FILING DATE: 1999-07-02

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Consensus

US-09-855-271-13

Query Match 100.0%; Score 35; DB 9; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 13 TDFTLTI 19

#### RESULT 3

US-09-828-708-95

; Sequence 95, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti

; FILE OF INVENTION: autoimmune disease

; FILE REFERENCE: 1361.005US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 95

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-828-708-95

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 13 TDFTLTI 19

#### RESULT 4

US-09-828-708-97

; Sequence 97, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti

; FILE OF INVENTION: autoimmune disease

; FILE REFERENCE: 1361.005US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97

; LENGTH: 32

; TYPE: PRT

US-09-828-708-97

; ORGANISM: Homo sapiens

US-09-828-708-97

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 13 TDFTLTI 19

#### RESULT 5

US-09-828-708-98

; Sequence 98, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti

; FILE OF INVENTION: autoimmune disease

; FILE REFERENCE: 1361.005US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 98

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-828-708-98

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 13 TDFTLTI 19

#### RESULT 6

US-09-828-708-100

; Sequence 100, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti

; FILE OF INVENTION: autoimmune disease

; FILE REFERENCE: 1361.005US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 100

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-828-708-100

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

Db 13 TDFTLTI 19

#### RESULT 7

US-09-828-708-101  
; Sequence 101, Application US/09828708  
; Patent No. US20020146753A1  
; GENERAL INFORMATION:  
; APPLICANT: Ditzel, H.  
; APPLICANT: Burton, D.  
; APPLICANT: Schaller, M.  
; TITLE OF INVENTION: Anticantibodies to glucose-6-phosphate isomerase and their partic  
; TITLE OF INVENTION: autoimmune disease  
; FILE REFERENCE: 1361.005051  
; CURRENT APPLICATION NUMBER: US/09/828,708  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 101  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-828-708-101

Query Match 100.0%; Score 35; DB 10; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7  
Db 13 TDFTLTI 19

RESULT 8  
US-09-949-559-91  
; Sequence 91, Application US/09949559  
; Patent No. US20020151682A1  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Brown, Derek Thomas  
; APPLICANT: Weir, Andrew Neil Charles  
; APPLICANT: Popplewell, Andrew George  
; APPLICANT: Chapman, Andrew Paul  
; APPLICANT: King, David John  
; TITLE OF INVENTION: Biological Products  
; FILE REFERENCE: Carp-0095  
; CURRENT APPLICATION NUMBER: US/09/949,559  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 0013810.7GB  
; PRIOR FILING DATE: 2000-06-06  
; PRIOR APPLICATION NUMBER: 09/875,221  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 91  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human group 1 consensus framework 13  
US-09-949-559-91

Query Match 100.0%; Score 35; DB 10; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7  
Db 13 TDFTLTI 19

RESULT 9  
US-09-949-559-92  
; Sequence 92, Application US/09949559  
; Patent No. US20020151682A1  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, Diljeet Singh

; APPLICANT: Brown, Derek Thomas  
; APPLICANT: Weir, Andrew Neil Charles  
; APPLICANT: Popplewell, Andrew George  
; APPLICANT: Chapman, Andrew Paul  
; APPLICANT: King, David John  
; TITLE OF INVENTION: Biological Products  
; FILE REFERENCE: Carp-0095  
; CURRENT APPLICATION NUMBER: US/09/949,559  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 0013810.7GB  
; PRIOR FILING DATE: 2000-06-06  
; PRIOR APPLICATION NUMBER: 09/875,221  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hTNP40 framework 13  
US-09-949-559-92

Query Match 100.0%; Score 35; DB 10; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7  
Db 13 TDFTLTI 19

RESULT 10  
US-09-874-141-15  
; Sequence 15, Application US/09874141  
; Publication No. US20030012781A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL  
; APPLICANT: PAN, LI-ZHEN  
; APPLICANT: HANNA, NABIL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: KLOETZER, WILLIAM S.  
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0280632  
; CURRENT APPLICATION NUMBER: US/09/874,141  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/209,584  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-141-15

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7  
Db 13 TDFTLTI 19

RESULT 11  
US-09-875-221A-91  
; Sequence 91, Application US/09875221A  
; Publication No. US20030026805A1  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Brown, Derek Thomas

APPLICANT: Weir, Andrew Neil Charles  
APPLICANT: Popplewell, Andrew George  
APPLICANT: Chapman, Andrew Paul  
APPLICANT: King, David John  
TITLE OF INVENTION: Biological Products  
FILE REFERENCE: Carp-0089  
CURRENT APPLICATION NUMBER: US/09/875,221A  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: GB0013810.7  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 91  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human group 1 consensus framework L3  
US-09-875-221A-91

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||  
DB 13 TDFTLTI 19

## RESULT 12

US-09-875-221A-92  
Sequence 92, Application US/09875221A  
Publication No. US20030026805A1  
GENERAL INFORMATION:  
APPLICANT: Achwal, Diljeet Singh  
APPLICANT: Brown, Derek Thomas  
APPLICANT: Weir, Andrew Neil Charles  
APPLICANT: Popplewell, Andrew George  
APPLICANT: Chapman, Andrew Paul  
APPLICANT: King, David John  
TITLE OF INVENTION: Biological Products  
FILE REFERENCE: Carp-0089  
CURRENT APPLICATION NUMBER: US/09/875,221A  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: GB0013810.7  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 92  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: hTNF4c framework L3  
US-09-875-221A-92

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||  
DB 13 TDFTLTI 19

## RESULT 13

US-09-563-222-76  
Sequence 76, Application US/C9563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Hein, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN

TITLE OF INVENTION: EUKARYOTIC CELLS  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 76  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-76

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||  
DB 13 TDFTLTI 19

## RESULT 14

US-09-563-222-84  
Sequence 84, Application US/09563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Hein, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
TITLE OF INVENTION: EUKARYOTIC CELLS  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 84  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-84

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
|||  
DB 13 TDFTLTI 19

## RESULT 15

US-09-563-222-88  
Sequence 88, Application US/09563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Hein, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
TITLE OF INVENTION: EUKARYOTIC CELLS  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 88  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-88

Query Match 100.0%; Score 35; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 TDFTLT 7  
13 TDFTLT 19

Search completed: October 4, 2003, 12:42:39  
Job time : 36.3333 secs

GenCore version 5.1.6  
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:18:51 ; Search time 17.6667 Seconds  
(without alignments)  
16.765 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4233858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : issued Patents AA:  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	25	5	PCT-US91-02942-42
2	35	100.0	32	2	US-08-470-139-13
3	35	100.0	32	3	US-08-569-147-40
4	35	100.0	32	4	US-09-347-061-13
5	35	100.0	32	4	US-09-425-638A-92
6	35	100.0	32	4	US-09-425-638A-94
7	35	100.0	32	4	US-09-543-004-92
8	35	100.0	32	4	US-09-543-004-94
9	35	100.0	50	5	PCT-US91-02942-9
10	35	100.0	52	1	US-08-162-102C-43
11	35	100.0	53	1	US-08-162-102C-44
12	35	100.0	64	2	US-08-765-1735-10
13	35	100.0	64	2	US-08-765-1735-14
14	35	100.0	70	3	US-08-554-840-9
15	35	100.0	70	4	US-08-925-339-9
16	35	100.0	70	4	US-08-925-339-9
17	35	100.0	76	3	US-08-851-362D-21
18	35	100.0	79	3	US-08-554-840-14
19	35	100.0	79	4	US-08-925-339-14
20	35	100.0	79	4	US-08-925-339-14
21	35	100.0	80	3	US-08-554-840-12
22	35	100.0	80	3	US-08-554-840-13
23	35	100.0	80	3	US-08-554-840-15
24	35	100.0	80	4	US-08-925-339-12
25	35	100.0	80	4	US-08-925-339-13
26	35	100.0	80	4	US-08-925-339-15
27	35	100.0	80	4	US-09-332-595-12

Sequence 13, Appl  
Sequence 15, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 49, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 35, Appl  
Sequence 35, Appl  
Sequence 11, Appl  
Sequence 6, Appl  
Sequence 3, Appl  
Sequence 6, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 4, Appl

ALIGNMENTS

RESULT 1  
PCT-US91-02942-42  
Sequence 42, Application: PC/TUS9102942  
GENERAL INFORMATION:  
APPLICANT: ROTHLEIN, ROBERT  
APPLICANT: ADAIR, JOHN R  
APPLICANT: ATHWAL, DILJEET S  
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Ave. NW Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02942  
FILING DATE: 19910429  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9009549.8  
FILING DATE: 27-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: FOX, SAM L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 1011.0586600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-02942-42

Query Match 100.0%; Score 35; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
Db 6 TDFTLTI 12

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RESULT 2
US-08-470-139-13
; Sequence 13, Application US/08470139
; Patent No. 598586
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDICAL TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,139
; FILING DATE: 06 JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-139-13

Query Match: 100.0%; Score 35; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLT 7
DB 13 TDFTLT 19

RESULT 3
US-08-569-147-40
; Sequence 40, Application US/08569147
; Patent No. 6180177
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: NO. 6180177, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDICAL TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

```

```

; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-569-147-40

Query Match: 100.0%; Score 35; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLT 7
DB 13 TDFTLT 19

RESULT 4
US-09-347-061-13
; Sequence 13, Application US/09347061
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match: 100.0%; Score 35; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLT 7
DB 13 TDFTLT 19

RESULT 5
US-09-425-638A-92
; Sequence 92, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LJD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-92

Query Match: 100.0%; Score 35; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Y 1 TDFTLTI 7  
13 TDFTLTI 19

ESULT 6  
S-09-425-638A-94  
Sequence 94, Application US/09425638A  
Patent No. 6342587  
GENERAL INFORMATION:  
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
APPLICANT: Lloyd J. Old  
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO  
FILE REFERENCE: LUD 5630  
CURRENT APPLICATION NUMBER: US/09/425.638A  
CURRENT FILING DATE: 1999-10-22  
NUMBER OF SEQ ID NOS: 129  
SEQ ID NO 94  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
S-09-425-638A-94

Query Match 100.0%; Score 35; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
13 TDFTLTI 19

ESULT 7  
S-09-543-004-92  
Sequence 92, Application US/09543004  
Patent No. 6346249  
GENERAL INFORMATION:  
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
APPLICANT: Lloyd J. Old  
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO  
FILE REFERENCE: LUD 5630.1  
CURRENT APPLICATION NUMBER: US/09/543.004  
CURRENT FILING DATE: 2000-04-04  
PRIOR APPLICATION NUMBER: 09/425.638  
PRIOR FILING DATE: 1999-10-22  
NUMBER OF SEQ ID NOS: 129  
SEQ ID NO 92  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
S-09-543-004-92

Query Match 100.0%; Score 35; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
13 TDFTLTI 19

ESULT 8  
S-09-543-004-94  
Sequence 94, Application US/09543004  
Patent No. 6346249  
GENERAL INFORMATION:  
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
APPLICANT: Lloyd J. Old  
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO  
FILE REFERENCE: LUD 5630.1  
CURRENT APPLICATION NUMBER: US/09/543.004

1 CURRENT FILING DATE: 2000-04-04  
2 PRIOR APPLICATION NUMBER: 09/425,638  
3 PRIOR FILING DATE: 1999-10-22  
4 NUMBER OF SEQ ID NOS: 129  
5 SEQ ID NO 94  
6 LENGTH: 32  
7 TYPE: PRT  
8 ORGANISM: Homo sapiens  
9 FEATURE:  
10 US-09-543-004-94

Query Match 100.0%; Score 35; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
13 TDFTLTI 19

RESULT 9  
PCT-US91-02942-9  
Sequence 9, Application PC/TUS9102942  
GENERAL INFORMATION:  
APPLICANT: ROTHLEIN, ROBERT  
APPLICANT: ADAIR, JOHN R  
APPLICANT: AHWAL, DILJEET S  
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED COM-1 ANTIBODY  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Ave. NW Suite 100  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DCS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02942  
FILING DATE: 19910429  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9009549.8  
FILING DATE: 27-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: FOX, SAM L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 101.05986600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US91-02942-9

Query Match 100.0%; Score 35; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
24 TDFTLTI 30

RESULT 10

US-08-162-102C-43  
Sequence 43, Application US/08162102C  
Patent No. 5762905  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R.  
APPLICANT: Barbas, III, Carlos F.  
APPLICANT: Chanock, Robert M.  
APPLICANT: Murphy, Brian R.  
APPLICANT: Crowe, Jr., James E.  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,102C  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07300/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-102C-43

Query Match 100.0%; Score 35; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLT 7  
| | | | |  
Db 13 TDFTLT 19

RESULT 11  
US-08-162-102C-44  
Sequence 44, Application US/08162102C  
Patent No. 5762905  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R.  
APPLICANT: Barbas, III, Carlos F.  
APPLICANT: Chanock, Robert M.  
APPLICANT: Murphy, Brian R.  
APPLICANT: Crowe, Jr., James E.  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,102C  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07300/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-102C-44

Query Match 100.0%; Score 35; DB 1; Length 53;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLT 7  
| | | | |  
Db 13 TDFTLT 19

RESULT 12  
US-08-765-179B-10  
Sequence 10, Application US/08765179B  
Patent No. 5854027  
GENERAL INFORMATION:  
APPLICANT: STEIPE, Boris  
APPLICANT: STEINBACHER, Stefan  
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
TITLE OF INVENTION: OF ANTIBODIES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Martelstein, Murray & Gram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,179B  
FILING DATE: 14-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/02626  
FILING DATE: 06-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 25 115.7  
FILING DATE: 15-JUL-1994  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein



S-08-765-179B-10

Query Match 100.0%; Score 35; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
:|||||  
b 38 TDFTLTI 44

RESULT 13

S-08-765-179B-14  
Sequence 14, Application US/08765179B  
Patent No. 5854027

GENERAL INFORMATION:

APPLICANT: STEIPE, Boris  
APPLICANT: STEINBEACHER, Stefan  
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
TITLE OF INVENTION: OF ANTIBODIES  
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,179B  
FILING DATE: 14-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02626

FILING DATE: 06-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 25 115.7

FILING DATE: 15-JUL-1994

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 64 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

S-08-765-179B-14

Query Match 100.0%; Score 35; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7  
:|||||  
b 38 TDFTLTI 44

RESULT 14

S-08-554-840-9  
Sequence 9, Application US/08554840  
Patent No. 6001358

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE: 07-NOV-1995  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-554-840-9

Query Match 100.0%; Score 35; DB 3; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
:|||||

Db 51 TDFTLTI 57

RESULT 15

US-08-925-339-9  
Sequence 9, Application US/08925339  
Patent No. 6440418  
GENERAL INFORMATION:  
APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/925,339  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE: 07-NOV-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin J.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: C12712-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 70 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-925-339-9

Query Match 100.0%; Score 35; DB 4; Length 70;  
 Best Local Similarity 100.0%; Pred. NO. 3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7  
 |||||  
 Db 51 TDFTLTI 57

Search completed: October 4, 2003, 12:27:22  
 Job time : 18.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:36 ; Search time 20.3333 Seconds  
(without alignments)  
33.107 Million cell updates/sec

Title: US-09-712-819C-6  
Perfect score: 33  
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168692 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	54	2 S34093	Ig kappa chain V r
2	33	100.0	71	2 H30538	Ig kappa chain V r
3	33	100.0	72	2 S40358	Ig kappa chain - h
4	33	100.0	75	2 S40337	Ig kappa chain V-J
5	33	100.0	83	2 S34095	Ig kappa chain V r
6	33	100.0	83	2 S24211	Ig kappa chain V r
7	33	100.0	87	2 S34091	Ig kappa chain V r
8	33	100.0	87	2 S34094	Ig kappa chain V r
9	33	100.0	89	2 B25155	Ig kappa chain V r
10	33	100.0	91	2 S42186	Ig kappa chain V r
11	33	100.0	91	2 S25463	Ig kappa chain V r
12	33	100.0	93	2 PH1039	Ig light chain V r
13	33	100.0	94	2 PL0258	Ig kappa chain V r
14	33	100.0	96	2 S40320	Ig kappa chain - h
15	33	100.0	99	2 S24501	Ig kappa chain V r
16	33	100.0	99	2 E28833	Ig heavy chain V r
17	33	100.0	99	2 S24504	Ig kappa chain V r
18	33	100.0	100	2 S26334	Ig light chain V r
19	33	100.0	100	2 S24681	Ig kappa chain - h
20	33	100.0	100	2 S45440	Ig kappa chain V r
21	33	100.0	101	2 PH1057	Ig light chain V r
22	33	100.0	101	2 C34153	Ig kappa chain V-I
23	33	100.0	101	2 A33730	Ig kappa chain V r
24	33	100.0	102	2 PH1035	Ig light chain V r
25	33	100.0	102	2 PH1044	Ig light chain V r
26	33	100.0	102	2 S14592	Ig kappa chain V r
27	33	100.0	102	2 E28195	Ig kappa chain V r
28	33	100.0	102	2 S14594	Ig kappa chain V r
29	33	100.0	102	2 S14593	Ig kappa chain V r

30	33	100.0	102	2 S14591	Ig kappa chain V r
31	33	100.0	102	2 S14590	Ig kappa chain V r
32	33	100.0	103	2 PH1034	Ig light chain V r
33	33	100.0	103	2 PH1036	Ig light chain V r
34	33	100.0	103	2 PH1037	Ig light chain V r
35	33	100.0	103	2 PH1038	Ig light chain V r
36	33	100.0	103	2 PH1040	Ig light chain V r
37	33	100.0	103	2 PH1041	Ig light chain V r
38	33	100.0	103	2 PH1042	Ig light chain V r
39	33	100.0	103	2 PH1043	Ig light chain V r
40	33	100.0	103	2 PH1045	Ig light chain V r
41	33	100.0	103	2 PH1055	Ig light chain V r
42	33	100.0	103	2 PH1056	Ig light chain V r
43	33	100.0	103	2 PH1098	Ig light chain V r
44	33	100.0	103	2 PH1099	Ig light chain V r
45	33	100.0	103	2 PH1100	Ig light chain V r

ALIGNMENTS

RESULT 1

S34093  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 07-May-1999  
C:Accession: S34093  
R:Wagner, S.D.; Luzzatto, J.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib  
A:Reference number: S34076; MUID:93170387; PMID:8436174  
A:Accession: S34093  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-54 <WAG>  
A:Cross-references: EMBL:X67177  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

Db 43 FTLKISR 49

RESULT 2

H30538  
Ig kappa chain V region (174.3F4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 09-May-1997  
C:Accession: H30538  
R:Claflin, J.L.; Berry, J.  
J. Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p  
A:Reference number: A30534; MUID:89035545; PMID:3141511  
A:Accession: H30538  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: mRNA  
A:Residues: 1-71 <CLA>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

Db 35 FTLKISR 41

```

RESULT 3
S40358
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40358
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40358
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <KLE>
A:Cross-references: EMBL:X72469; NID:G441404; PID:CAA51136.1; PID:G441405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 28 FTLKISR 34

RESULT 4
S40337
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40337
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40337
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-75 <KLE>
A:Cross-references: EMBL:X72447; NID:G441362; PID:CAA51115.1; PID:G441363
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 30 FTLKISR 36

RESULT 5
S34095
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34095
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 63 FTLKISR 69

RESULT 6
S24211
Ig kappa chain V region (V3a) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24211
R:Pargent, W.; Meindl, A.; Thiebe, R.; Mitzei, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated C kappa
A:Reference number: S24205; MUID:9330953; PMID:1907917
A:Accession: S24211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <PAR>
A:Cross-references: EMBL:X59317; NID:G33270; PID:CAA42004.1; PID:G33271
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 59 FTLKISR 65

RESULT 7
S34091
Ig kappa chain V region (patient 19 and 20) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S34091; S34092
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34091
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67175
A:Experimental source: patient 19
A:Accession: S34092
A:Molecule type: DNA
A:Residues: 1-87 <WAW>
A:Cross-references: EMBL:X67176
A:Experimental source: patient 20
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 63 FTLKISR 69

RESULT 8
S34094

```

```

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34094
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: EMBL:X67178
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-82/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 63 FTLKISR 69

RESULT 9
S25155
Ig kappa chain V region (SM1.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 02-Jun-1988 #text_change 16-Aug-1996
C;Accession: B25155
R;Robbins, P.F.; Rosen, E.M.; Haba, S.; Nisenooff, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1050-1054, 1986
A;Title: Relationship of V(H) and V(L) genes encoding three idiotypic families of anti-p
A;Reference number: A94083; MUID:86149212; PMID:3081888
A;Accession: B25155
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-89 <ROB>
C;Comment: This chain is expressed in an Igm with anti-arsenate activity.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 54 FTLKISR 60

RESULT 10
S42186
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S42186; S42195
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <MOJ>
A;Cross-references: EMBL:Z25442; NID:9407830; PIDN:CAA90929.1; PID:9407831
A;Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85 a
A;Accession: S42195
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <MO2>

A;Cross-references: EMBL:Z25460; NID:9407848; PIDN:CAA80947.1; PID:9407849
A;Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-86/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 67 FTLKISR 73

RESULT 11
S25463
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25463
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histo
A;Reference number: S25174
A;Accession: S25463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <MON>
A;Cross-references: EMBL:X67624; NID:952189; PIDN:CAA47883.1; PID:9238264
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 76 FTLKISR 82

RESULT 12
PH1039
Ig light chain V region (clone 165.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C;Accession: PH1039
R;Tillman, D.W.; Jou, N.T.; Hill, R.C.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective E
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1039
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-93 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 67 FTLKISR 73

RESULT 13
PL0258
Ig kappa chain V region (anti-DNA, 1581VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
```

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C;Accession: P0258  
C;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 245-297, 1990  
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A;Reference number: P0231; MUID:90111616; PMID:2104919  
A;Accession: P0258  
A;Molecule type: mRNA  
A;Residues: 1-94 <SHL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-6/Region: framework 1  
F;7-22/Region: complementarity-determining 1  
F;23-37/Region: framework 2  
F;38-44/Region: complementarity-determining 2  
F;45-76/Region: framework 3  
F;77-85/Region: complementarity-determining 3  
F;86-94/Region: framework 4

Query Match 100.0%; Score 33; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLKISR 7  
|||  
Db 59 FTLKISR 65

RESULT 14  
S40320  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C;Accession: S40320  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40320  
A;Status: preliminary; translation not shown.  
A;Molecule type: mRNA  
A;Residues: 1-96 <KLE>  
A;Cross-references: EMBL:X72430; NID:9441328; PID:CAA51096.1; PID:9441329  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLKISR 7  
|||  
Db 59 FTLKISR 65

RESULT 15  
S24501  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S24501  
R;Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A;Reference number: S24490  
A;Accession: S24501  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-99 <KAA>  
A;Cross-references: EMBL:X66639  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 33; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY : 1 FTLKISR 7  
|||  
Db 76 FTLKISR 82

Search completed: October 4, 2003, 12:26:21  
Job time : 20.3333 secs.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:51 ; Search time 13.6667 Seconds  
(without alignments)  
30.861 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	112	1 KV2C_HUMAN	P01616 homo sapien
2	33	100.0	113	1 KV2D_HUMAN	P01617 homo sapien
3	33	100.0	113	1 KV2G_MOUSE	P01631 mus musculus
4	33	100.0	115	1 KV2A_HUMAN	P01614 homo sapien
5	33	100.0	117	1 KV2E_HUMAN	P06309 homo sapien
6	33	100.0	133	1 KV2F_HUMAN	P06310 homo sapien
7	30	90.9	112	1 KV2D_MOUSE	P01629 mus musculus
8	30	90.9	113	1 KV2B_HUMAN	P01615 homo sapien
9	30	90.9	113	1 KV2E_MOUSE	P03976 mus musculus
10	30	90.9	113	1 KV2F_MOUSE	P01630 mus musculus
11	30	90.9	512	1 ANM3_HUMAN	O60678 homo sapien
12	30	90.9	772	1 CIPB_CLOTM	Q01866 clostridium
13	30	90.9	1853	1 CIPA_CLOTM	Q06851 clostridium
14	29	87.9	112	1 KV2A_MOUSE	P01626 mus musculus
15	29	87.9	113	1 KV2C_MOUSE	P01628 mus musculus
16	29	87.9	120	1 KV2B_MOUSE	P01627 mus musculus
17	29	87.9	834	1 PLSB_PSEAE	Q9hxx7 pseudomonas
18	28	84.8	259	1 Y068_CHLTR	Q84071 chlamydia t
19	28	84.8	259	1 Y339_CHLMC	Q9pax1 chlamydia m
20	28	84.8	711	1 CAD2_LISMO	Q60048 listeria mo
21	28	84.8	745	1 ATK2_ARATH	P46864 arabidopsis
22	27	81.8	100	1 KV3C_HUMAN	P01621 homo sapien
23	27	81.8	108	1 KV3A_HUMAN	P01619 homo sapien
24	27	81.8	109	1 KV3B_HUMAN	P01620 homo sapien
25	27	81.8	109	1 KV3D_HUMAN	P01622 homo sapien
26	27	81.8	109	1 KV3E_HUMAN	P01623 homo sapien
27	27	81.8	109	1 KV3F_HUMAN	P04206 homo sapien
28	27	81.8	127	1 YJ07_YEAST	P47105 saccharomyc
29	27	81.8	129	1 KV3H_HUMAN	P04207 homo sapien
30	27	81.8	129	1 KV3L_HUMAN	P18135 homo sapien
31	27	81.8	129	1 KV3M_HUMAN	P18136 homo sapien
32	27	81.8	295	1 YH08_YEAST	P38805 saccharomyc
33	27	81.8	239	1 ATNC_BUFXA	P43002 bufo marinu

34	27	81.8	362	1 RECF_PROMI	P22839 proteus mir
35	27	81.8	437	1 RUMA_PASMU	Q9CJX3 pasteurella
36	27	81.8	123	1 KF4A_MOUSE	P35174 mus musculus
37	27	81.8	1232	1 KF4A_HUMAN	O95239 homo sapien
38	27	81.8	1541	1 NX3A_HUMAN	Q9Y4C0 homo sapien
39	27	81.8	1578	1 NX3A_RAT	Q07310 rattus norv
40	27	81.8	2065	1 T2D1_DROME	P51123 drosophila
41	26	78.8	108	1 KVI_CANFA	P01618 canis famil
42	26	78.8	172	1 RIMM_STRP3	Q8K7X4 streptococc
43	26	78.8	172	1 RIMM_STRP9	Q8P1F4 streptococc
44	26	78.8	172	1 RIMM_STRPY	P58183 streptococc
45	26	78.8	194	1 Y4HQ_RHISN	P50361 rhizobium s

ALIGNMENTS

RESULT 1  
KV2C\_HUMAN  
ID KV2C\_HUMAN STANDARD; PRT; 112 AA.  
AC P01616;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region M1.  
CS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA Dreyer W.C., Gray W.R., Hood L.E.;  
RT "The genetic, molecular, and cellular basis of antibody formation:  
RT some facts and a unifying hypothesis.";  
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
DR PIR; AC1887; K2HUML.  
DR HSSP; P80362; 1WT.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 39 53 FRAMEWORK-2  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 61 92 FRAMEWORK-3  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 111 FRAMEWORK-4  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE491 CRC64;  
Query Match 100.0%; Score 33; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
DB . 75 FTLKISR 81  
RESULT 2  
KV2D\_HUMAN  
ID KV2D\_HUMAN STANDARD; PRT; 113 AA.  
AC P01617;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region TEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE (BENCE-JONES PROTEIN TEW).  
RP MEDLINE=74148480; PubMed=4596149;  
RX Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
RA "Amino acid sequence of a kappa Bence Jones protein from a case of  
RT primary amyloidosis.";  
RL Biochemistry 12:3763-3780(1973).  
RN [2]  
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RX MEDLINE=73166638; PubMed=4700495;  
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,  
RA Glenner G.G.;  
RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
RT patient with plasma cell dyscrasia and amyloidosis.";  
RL J. Clin. Invest. 52:1276-1281(1973).  
CC -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL  
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.  
CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A  
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (2.2)  
CC MARKER.  
CC PIR; A90370; K2HUTW.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
DR Immunoglobulin V region; Bence-Jones protein; Amyloid.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 40 54 FRAMEWORK-2.  
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 62 93 FRAMEWORK-3.  
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 103 112 FRAMEWORK-4.  
FT DISULFID 23 93 BY SIMILARITY.  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12316 MW; 00103AF81F1843CA CRC64;  
Query Match 100.0%; Score 33; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 76 FTLKISR 82  
RESULT 3  
KV2G\_MOUSE STANDARD; PRT; 113 AA.  
ID KV2G\_MOUSE  
AC P01631;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region 26-10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE.  
RP STRAIN=A/J;  
Query Match 100.0%; Score 33; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 76 FTLKISR 82  
RESULT 4  
KV2A\_HUMAN STANDARD; PRT; 115 AA.  
ID KV2A\_HUMAN  
AC P01614;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region Cum.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE.  
RP MEDLINE=68242259; PubMed=5586923;  
RX Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
RT type).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 346:1718-1722(1967).  
RN [2]  
RP REVISIONS TO 50; 52; 96 AND 97.  
RX MEDLINE=70063440; PubMed=4188189;  
RA Hilschmann N.;  
RT "Molecular basis of antibody formation.";  
RL Naturwissenschaften 56:195-205(1969).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; B91639; K2HUCM.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGv; 1.

RX MEDLINE=83178921; PubMed=6404298;  
RA Novotny J., Margolies M.N.;  
RT "Amino acid sequence of the light chain variable region from a mouse  
RT anti-digoxin hybridoma antibody.";  
RL Biochemistry 22:1153-1158(1983).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA  
CC PROTEIN THAT BINDS DIGOXIN.  
DR PIR; A01914; KVM526.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 40 54 FRAMEWORK-2.  
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 62 93 FRAMEWORK-3.  
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 103 112 FRAMEWORK-4.  
FT DISULFID 23 93 BY SIMILARITY.  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;  
Query Match 100.0%; Score 33; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 76 FTLKISR 82



DR PROSITE; PSS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
TT DISULFID 24 95 BY SIMILARITY.  
TT NON TER 115 115  
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;  
  
Query Match 100.0%; Score 33; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLKISR 7  
Db 78 FTLKISR 84  
  
RESULT 5  
KV2E HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
E Ig kappa chain V-II region G607 precursor (Fragment).  
DS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
CC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=5125927;  
RA Klobbeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain  
diversity";  
RL Nature 309:73-76 (1994).  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; Z00009; -; NOT\_ANNOTATED\_CDS.  
CC PIR; A01889; K2HJGM.  
CC HSSP; P80362; 1WTJ.  
CC GO; GO:0005576; C:extracellular; NAS.  
CC GO; GO:0003823; F:antigen binding activity; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003006; Ig\_MHC.  
CC Pfam; PF00047; Ig\_v.  
CC SMART; SM00406; IGv; 1.  
CC PROSITE; PSS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
TT NON TER 1 4  
TT SIGNAL <1 4  
TT CHAIN 5 117 IG KAPPA CHAIN V-II REGION G607.  
TT DOMAIN 5 27 FRAMEWORK-1.  
TT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.  
TT DOMAIN 44 59 FRAMEWORK-2.  
TT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.  
TT DOMAIN 66 97 FRAMEWORK-3.  
TT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.  
TT DOMAIN 107 117 FRAMEWORK-4.  
TT DISULFID 27 97 BY SIMILARITY.  
TT NON TER 117 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC713E5558B1 CRC64;  
  
Query Match 100.0%; Score 33; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
Db 80 FTLKISR 86  
  
RESULT 6  
KV2F HUMAN STANDARD; PRT; 133 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
E Ig kappa chain V-II region RPMI 6410 precursor.  
DS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
CC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86041852; PubMed=2997711;  
RA Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and  
III";  
RL Nucleic Acids Res. 13:6499-6513 (1985).  
CC  
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CC  
CC EMBL; Z00020; CAA77315.1; -  
CC PIR; A01890; K2HURP.  
CC HSSP; P80362; 1WTJ.  
CC GO; GO:0005576; C:extracellular; NAS.  
CC GO; GO:0003823; F:antigen binding activity; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_v.  
CC Pfam; PF00047; Ig; 1.  
CC SMART; SM00406; IGv; 1.  
CC PROSITE; PSS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
TT SIGNAL 1 20  
TT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.  
TT DOMAIN 21 43 FRAMEWORK-1.  
TT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.  
TT DOMAIN 60 74 FRAMEWORK-2.  
TT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
TT DOMAIN 82 113 FRAMEWORK-3.  
TT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.  
TT DOMAIN 123 132 FRAMEWORK-4.  
TT DISULFID 43 113 BY SIMILARITY.  
TT NON TER 133 133  
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;  
  
Query Match 100.0%; Score 33; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLKISR 7  
Db 96 FTLKISR 102  
  
RESULT 7  
KV2D MOUSE STANDARD; PRT; 112 AA.  
ID KV2D MOUSE  
AC P01629;

DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region 2S1.3.  
CS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83055101; PubMed=7141411;  
RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;  
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for  
the group A streptococcal polysaccharide."  
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076 (1982).  
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
DR PIR; A01911; KVMSS1.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Monoclonal antibody.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;  
Query Match 90.9%; Score 30; DB 1; Length 112;  
Best Local Similarity 85.7%; Pred. No. 1.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 76 FTLRISR 82

RESULT 8  
KV2B\_HUMAN  
ID \_KV2B\_HUMAN STANDARD; PRT; 113 AA.  
AC P01615;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region FR.  
CS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76253627; PubMed=821524;  
RA Riesen W.F., Jaton J.-C.;  
RT "Variable region sequence of the light chain from a Waldenstrom's IgM  
with specificity for phosphorylcholine."  
RL Biochemistry 15:3829-3833 (1976).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
DR PIR; A01886; K2HUF.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; Extracellular; NAS.  
DR GO; GO:0003923; F-antigen binding activity; NAS.  
DR GO; GO:0006955; Immune response; NAS.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;  
Query Match 90.9%; Score 30; DB 1; Length 113;  
Best Local Similarity 85.7%; Pred. No. 2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 76 FTLKISR 82

RESULT 9  
KV2E\_MOUSE  
ID \_KV2E\_MOUSE STANDARD; PRT; 113 AA.  
AC P03976;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region 17S29.1.  
CS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85128968; PubMed=6441768;  
RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;  
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6  
origin: monoclonal antibodies 17S29.1 and 2S25.1 specific for the  
group A-streptococcal polysaccharide."  
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383 (1984).  
CC -!- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.  
DR PIR; A01912; KVMSS17.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8D533 CRC64;  
Query Match 90.9%; Score 30; DB 1; Length 113;  
Best Local Similarity 85.7%; Pred. No. 2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7

```
Db 76 FTLRISR 52
|||||
RESULT 10
KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region (S34.1).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409069;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC
DR PIR; A01913; KMS78.
DR HSSP; P80362; LNTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00935; IGLIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 113;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLKISR 7
|||||
Db 76 FTLRISR 82

RESULT 11
ANM3 HUMAN STANDARD; PRT; 512 AA.
AC O60678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein arginine N-methyltransferase 3 (EC 2.1.1.1-) (Fragment).
GN PRMT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9642256;
RX MEDLINE=96307932;

RA Tang J., Gary J.D., Clarke S., Herschman H.R.;
RT "PRMT 3, a type I protein arginine N-methyltransferase that differs
RT from PRMT1 in its oligomerization, subcellular localization,
RT substrate specificity, and regulation."
RL J. Biol. Chem. 273:16935-16945(1998).
CC -!- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE
CC GUANIDINO NITROGENS OF ARGINYL RESIDUES IN SOME PROTEINS.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
CC FAMILY.
CC
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CC
CC EMBL; AF059531; AAC39837.1; -.
CC XIM; 603190; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0016274; F:protein-arginine N-methyltransferase activity; NAS.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR007087; ZnF_C2H2.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS00028; ZINC FINGER C2H2_1; UNKNOWN_1.
KW Transferase; Methyltransferase; Zinc-finger.
FT NON TER 1
FT ZN FING 29 52 C2H2-TYPE.
SQ SEQUENCE 512 AA; 58098 MW; 260DC4EB25162A18 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 512;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 FTLKISR 7
|||||
Db 419 FTLKISR 425

RESULT 12
CIPB CLOTH STANDARD; PRT; 772 AA.
AC Q01866;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellulosomal scaffolding protein B (Cellulosomal glycoprotein S1/SL)
DE (Cellulose integrating protein B) (Fragment).
GN CIPB.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=YS;
RX MEDLINE=93146373; PubMed=1490597;
RA Poole J.M., Morag E., Lamed R., Bayer E.A., Hazlewood G.P.,
RA Gilbert H.J.;
RT "Identification of the cellulose-binding domain of the cellulosome
RT subunit S1 from Clostridium thermocellum YS."
RL FEMS Microbiol. Lett. 78:181-186(1992).
CC -!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSE. IT
CC PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CC CELLULOLYTIC ENZYMES PROBABLY THROUGH THE BINDING OF THE NINE
CC REPEATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS
CC PRESENT IN CATALYTIC SUBUNITS OF THE CELLULOSE.
CC -!- SUBCELLULAR LOCATION: CELL SURFACE.
CC -!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
CC THE CATALYTIC COMPONENTS OF THE CELLULOSE.
```

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CC -!- SIMILARITY: Contains at least 3 cohesin domains.
CC -!- SIMILARITY: Contains 2 dockerin domains.
CC -----
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CC -----
CC EMBL; X68233; CAA48312.1; -.
CC HSSP; Q36851; INBC.
CC InterPro; IPR001956; CBD_3.
CC InterPro; IPR002102; Cohesin.
CC InterPro; IPR002105; Dockerin_1.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00942; CBM_3; 1.
CC Pfam; PF00963; Cohesin; 3.
CC Pfam; PF00404; Dockerin_1; 2.
CC ProDom; PD001947; CBD_3; 1.
CC PROSITE; PS00018; EF_HAND; UNKNOWN_1.
CC PROSITE; PS00448; CLOS_CELLULOSE_RPT; 2.
CC KX Cellulose degradation; Cell wall; Glycoprotein; Repeat.
FT NON_TER 1
FT DOMAIN <1 80 COHESIN 1.
FT DOMAIN 81 93 LINKER (PRO/THR-RICH).
FT DOMAIN 94 240 COHESIN 2.
FT DOMAIN 241 272 LINKER (PRO/THR-RICH).
FT DOMAIN 273 439 CELLULOSE-BINDING.
FT DOMAIN 440 461 LINKER (PRO/THR-RICH).
FT DOMAIN 462 607 COHESIN 3.
FT DOMAIN 710 733 DOCKERIN 1.
FT DOMAIN 743 766 DOCKERIN 2.
SQ SEQUENCE 772 AA; 82491 MW; BFF06DESE094FE10 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 772;
Best Local Similarity 85.7%; Pred.No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 672 YTLKISR 678

RESULT 13
CIPA_CLOTH STANDARD; PRT; 1853 AA.
AC Q06851;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellulosomal scaffolding protein A precursor (Cellulosomal
DE glycoprotein S1/S1) (Cellulose integrating protein A) (Cohesin).
CN CIPA.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-40 AND 42-43.
RC STRAIN=ATCC 27405 / DSM 1237;
RX MEDLINE=93302508; PubMed=9316083;
RA Gerngross U.T., Romaniec M.P.M., Kobayashi T., Huskisson N.S.,
RA Demain A.L.;
RT "Sequencing of a Clostridium thermocellum gene (cipA) encoding the
RT cellulosomal SL-protein reveals an unusual degree of internal
RT homology."
RL Mol. Microbiol. 8:325-334(1993).
RN (2)
RP SEQUENCE OF 1820-1853 FROM N.A.
RX MEDLINE=93209931; PubMed=8458832;
RA Fujino T., Beguin P., Aubert J.-P.;
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RT "Organization of a Clostridium thermocellum gene cluster encoding the
RT cellulosomal scaffolding protein Cipa and a protein possibly involved
RT in attachment of the cellulosome to the cell surface."
RL J. Bacteriol. 175:1891-1899(1993).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 184-321.
RX MEDLINE=97238934; PubMed=9083107;
RA Shimizu L.J.W., Bayer E.A., Morag E., Lamed R., Yaron S., Shoham Y.,
RA Frolow F.;
RT "A cohesin domain from Clostridium thermocellum: the crystal
RT structure provides new insights into cellulosome assembly."
RL Structure 5:381-390(1997).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 368-522.
RX MEDLINE=97076134; PubMed=8918451;
RA Torino J., Lamed R., Chirino A.J., Morag E., Bayer E.A., Shoham Y.,
RA Steitz T.A.;
RT "Crystal structure of a bacterial family-III cellulose-binding
RT domain: a general mechanism for attachment to cellulose."
RL EMBO J. 15:5739-5751(1996).
RN (5)
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1213-1361.
RX MEDLINE=98022914; PubMed=9402065;
RA Tavares G.A., Beguin P., Alzari P.M.;
RT "The crystal structure of a type I cohesin domain at 1.7-A
RT resolution."
RL J. Mol. Biol. 273:701-713(1997).
CC -!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSE. IT
CC PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CC CELLULOLYTIC ENZYMES.
CC -!- SUBCELLULAR LOCATION: CELL SURFACE.
CC -!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
CC THE CATALYTIC COMPONENTS OF THE CELLULOSE.
CC -!- SIMILARITY: Contains 9 cohesin domains.
CC -!- SIMILARITY: Contains 2 dockerin domains.
CC -----
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CC -----
CC EMBL; L08665; -. NOT ANNOTATED_CDS.
CC EMBL; X67506; CAA47840.1; -.
CC PIR; S36859; S36859.
CC PDB; 1ANU; 23-JUL-97.
CC PDB; 1AOH; 08-JUL-98.
CC PDB; INBC; 26-SEP-97.
CC InterPro; IPR001956; CBD_3.
CC InterPro; IPR002102; Cohesin.
CC InterPro; IPR002105; Dockerin_1.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00942; CBM_3; 1.
CC Pfam; PF00963; Cohesin; 3.
CC Pfam; PF00404; Dockerin_1; 2.
CC ProDom; PD001947; CBD_3; 1.
CC PROSITE; PS00018; EF_HAND; UNKNOWN_1.
CC PROSITE; PS00448; CLOS_CELLULOSE_RPT; 2.
CC Cellulose degradation; Cell wall; Glycoprotein; Repeat; Signal;
CC 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 1853 CELLULOSONAL SCAFFOLDING PROTEIN A.
FT DOMAIN 29 182 COHESIN 1.
FT DOMAIN 183 322 COHESIN 2.
FT DOMAIN 323 363 LINKER (PRO/THR-RICH).
FT DOMAIN 364 522 CELLULOSE-BINDING (BY SIMILARITY).
FT DOMAIN 523 559 LINKER (PRO/THR-RICH).
FT DOMAIN 560 704 COHESIN 3.
FT DOMAIN 724 866 COHESIN 4.
FT DOMAIN 889 1031 COHESIN 5.
FT DOMAIN 1054 1196 COHESIN 6.
```

FT DOMAIN 1219 1361  
FT DOMAIN 1384 1526  
FT DOMAIN 1548 1690  
FT DOMAIN 1791 1814  
FT DOMAIN 1824 1847  
FT CONFLICT 1615 1615  
FT STRAND 185 188  
FT STRAND 190 191  
FT TURN 195 196  
FT STRAND 198 206  
FT TURN 210 211  
FT STRAND 213 221  
FT TURN 224 226  
FT STRAND 227 234  
FT TURN 236 237  
FT TURN 243 246  
FT STRAND 247 252  
FT TURN 253 256  
FT STRAND 257 263  
FT TURN 265 266  
FT TURN 270 271  
FT STRAND 273 273  
FT STRAND 277 286  
FT STRAND 292 304  
FT TURN 305 306  
FT STRAND 309 309  
FT STRAND 313 315  
FT STRAND 317 319  
FT STRAND 369 375  
FT STRAND 381 382  
FT STRAND 385 385  
FT STRAND 397 397  
FT STRAND 399 400  
FT HELIX 401 403  
FT STRAND 404 404  
FT STRAND 418 428  
FT TURN 430 431  
FT STRAND 434 436  
FT HELIX 438 440  
FT STRAND 441 452  
FT TURN 453 454  
FT STRAND 455 463  
FT STRAND 467 468  
FT TURN 470 471  
FT STRAND 473 482  
FT TURN 483 484  
FT STRAND 488 489  
FT TURN 491 492  
FT TURN 494 495  
FT STRAND 498 498  
FT STRAND 503 504  
FT STRAND 509 512  
FT TURN 513 514  
FT STRAND 515 518  
FT STRAND 1220 1224  
FT STRAND 1226 1229  
FT TURN 1231 1232  
FT STRAND 1234 1242  
FT TURN 1246 1247  
FT STRAND 1249 1249  
FT STRAND 1251 1257  
FT TURN 1260 1262  
FT STRAND 1263 1270  
FT TURN 1272 1273  
FT HELIX 1279 1282  
FT STRAND 1283 1288  
FT STRAND 1289 1292  
FT STRAND 1293 1299  
FT TURN 1301 1302  
FT TURN 1306 1307  
FT STRAND 1309 1309  
FT STRAND 1313 1322  
FT TURN 1324 1325

COHESIN 7.  
COHESIN 8.  
COHESIN 9.  
DOCKERIN 1.  
DOCKERIN 2.  
A -> AA (IN REF. 1).  
FT STRAND 1329 1342  
FT TURN 1344 1345  
FT STRAND 1348 1348  
FT STRAND 1351 1354  
FT STRAND 1356 1360  
SQ SEQUENCE 1853 AA; 196831 MW; 3ABDDC03ABFC5372 CRC64;  
Query Match 90.9%; Score 30; DB 1; Length 1853;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FTLKISR 7  
Db 1753 YTLKISR 1759  
RESULT 14  
KV2A\_MOUSE  
ID KV2A\_MOUSE STANDARD; PRT; 112 AA.  
AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-1; region MOPC 167.  
OS Mus musculus (Mouse).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S., Potter M.;  
RT "Kappa Chain variable region from M167, a phosphorylcholine binding  
RT myeloma protein."  
RL Biochemistry 17:2703-2707(1978).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY  
CC CHAIN HAS ALSO BEEN DETERMINED.  
DR PIR; A01908; KVM516.  
DR HSSP; P8C362; 1WTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD64C4B9726 CRC64;  
Query Match 87.9%; Score 29; DB 1; Length 112;  
Best Local Similarity 85.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FTLKISR 7  
Db 76 FTLEISR 82  
RESULT 15  
KV2C\_MOUSE  
ID KV2C\_MOUSE STANDARD; PRT; 113 AA.  
AC P01628;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)  
DE Ig kappa chain V-1 region MOPC 511.  
OS Mus musculus (Mouse).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81052016; PubMed=6776396;  
RA Appella E.;  
RT "Amino acid sequence of the light chain variable region of Mb11, a  
RT phosphorylcholine-binding murine myeloma protein.";  
RL Mol. Immunol. 17:711-718(1980).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE.  
DR PIR; A01910; KVM551.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12496 MW; EFBDC4DA2BD3450 CRC64;  
FRAMEWORK-1.  
COMPLEMENTARITY-DETERMINING-1.  
FRAMEWORK-2.  
COMPLEMENTARITY-DETERMINING-2.  
FRAMEWORK-3.  
COMPLEMENTARITY-DETERMINING-3.  
FRAMEWORK-4.  
BY SIMILARITY.

Query Match 87.9%; Score 29; DB 1; Length 113;  
Best Local Similarity 55.7%; Pred. No. 3.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTCKISR 7  
| | | | |  
Db 76 FTLEISR 92

Search completed: October 4, 2003, 12:22:38  
Job time : 12.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:13 ; Search time 49.6667 Seconds  
(without alignments)  
36.370 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	104	11 Q9JL82	Q9JL82 mus musculu
2	33	100.0	114	4 Q9UL80	Q9UL80 homo sapien
3	33	100.0	148	11 Q8K122	Q8K122 mus musculu
4	33	100.0	238	11 Q8VC16	Q8VC16 mus musculu
5	33	100.0	238	11 Q99M37	Q99M37 mus musculu
6	33	100.0	239	11 Q8VC55	Q8VC55 mus musculu
7	33	100.0	239	11 Q8K3F8	Q8K3F8 mus musculu
8	30	90.9	239	4 Q8NEK0	Q8NEK0 homo sapien
9	30	90.9	239	4 Q8TDC0	Q8TDC0 homo sapien
10	30	90.9	548	4 Q8WJV3	Q8WJV3 homo sapien
11	30	90.9	638	2 Q46453	Q46453 clostridium
12	30	90.9	764	5 Q8IKT5	Q8IKT5 plasmodium
13	30	90.9	3848	5 Q76737	Q76737 dictyosteli
14	28	84.8	31	2 Q9R4X1	Q9R4X1 treponema d
15	28	84.8	80	2 Q9FAA7	Q9FAA7 brevibacter
16	28	84.8	80	2 Q9FDR9	Q9FDR9 corynebacte

Q8nr52 corynebacte  
Q9rv56 staphylococ  
Q9rwy8 deinococcus  
Q8iwc9 homo sapien  
Q9cu48 mus musculu  
Q95y35 caenorhabdi  
Q9cu16 mus musculu  
Q93xf8 zea mays (m  
Q25171 helicobacte  
Q92xg8 helicobacte  
Q56257 treponema d  
Q9vci7 drosophila  
Q9tzg7 caenorhabdi  
Q9nw40 homo sapien  
Q99y28 streptococc  
Q926c7 rhizobium m  
Q8cqn7 staphylococ  
Q52149 synecococc  
Q949g8 malus flori  
Q949g9 malus flori  
Q9tx96 drosophila  
Q973a6 sulfolobus  
Q8d127 yersinia pe  
Q9ui86 homo sapien  
Q9ui78 homo sapien  
Q38915 saccharomyc  
Q8y7e9 listeria mc  
Q9c8p6 arabidopsis  
Q9kmi2 vibrio chol

ALIGNMENTS

RESULT 1  
Q9JL82  
ID Q9JL82 PRELIMINARY; PRT; 104 AA.  
AC Q9JL82;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Maikiel S., Liao L., Cunningham M.W., Diamond R.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin.";  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206024; AAF69322.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 104  
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBD5F0AA1AE CRC64;  
  
Query Match 100.0%; Score 33; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLKISR 7

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DR Pfam; PF00047; i9; 2.
DR SMART; SM00406; iGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEEC3A3B03871D CRC64;

Query Match
Best Local Similarity 90.9%; Score 30; DB 4; Length 239;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 96 FTLKISR 102

RESULT 10
Q8WUV3 PRELIMINARY; PRT; 548 AA.
AC Q8WUV3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TSSJE=Muscie;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/CCSJ databases.
DR EMBL; ACC19339; AAH19339.1; -.
DR InterPro; IPR000051; SAM_bind.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 548 AA; 61967 MW; 11F5A3F52B105F56 CRC64;

Query Match
Best Local Similarity 90.9%; Score 30; DB 4; Length 548;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 455 FTLKISR 461

RESULT 11
Q46453 PRELIMINARY; PRT; 638 AA.
AC Q46453;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cipa protein (Fragment).
GN CIPA.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujino T., Beguin P., Aubert J.P.;
RT "Cloning of a Clostridium thermocellum DNA fragment encoding
RL polypeptides that bind the catalytic components of the cellulosome.";
RN [2]
RP SEQUENCE FROM N.A.
RX M5CLINE=92394486; PubMed=1521765;
RA Fujino T., Beguin P., Aubert J.P.;
RT "Cloning of a Clostridium thermocellum DNA fragment encoding
RT polypeptides that bind the catalytic components of the cellulosome.";
```

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RJ FEMS Microbiol. Lett. 73:165-170(1992).
DR EMBL; X67406; CAA47806.1; -.
DR HSSP; Q06851; IACH.
DR InterPro; IPR002102; Cchesin.
DR InterPro; IPR002105; Dockerin_1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF03963; Cohesin; 3.
DR Pfam; PF03404; Dockerin_1; 2.
DR PROSITE; PS00448; CLOS_CELLULOsome_RPT; 2.
DR PROSITE; PS00018; EF_HAND; 1.
FT NON_TER 1
SQ SEQUENCE 638 AA; 68255 MW; 355C17E50AFCCBE6 CRC64;

Query Match
Best Local Similarity 90.9%; Score 30; DB 2; Length 638;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 538 YTLKISR 544

RESULT 12
Q8IKT5 PRELIMINARY; PRT; 764 AA.
ID Q8IKT5
AC Q8IKT5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Peptidase, putative.
GN PF14_0517.
CS Plasmodium falciparum (isolate 3D7).
CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shalimov S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings J.M., Subramanian G.M., Mungaii C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RC falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AEO14824; AAN37130.1; -.
SQ SEQUENCE 764 AA; 88502 MW; 8BD974E0F9B2BC34C CRC64;

Query Match
Best Local Similarity 90.9%; Score 30; DB 5; Length 764;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 199 FTLRISR 205

RESULT 13
O76737 PRELIMINARY; PRT; 3648 AA.
ID O76737
AC O76737;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TIPC.
GN TIPC.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
```



OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=99331084; PubMed=10402673;  
RA Stege J.T., Laub M.T., Loomis W.F.;  
RT "tip genes act in parallel pathways of early Dictyostelium  
RT development."; 25:64-77(1999).  
RL Dev. Genet. 25:64-77(1999).  
DR EXBL: AF079445; AAC31916.1;  
SQ SEQUENCE 3848 AA; 440033 MW; 65B671566F7AE534 CRC64;

Query Match 90.9%; Score 30; DB 5; Length 3848;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|||  
Db 886 FTLKISK 892

RESULT 14

Q9R4X1 PRELIMINARY; PRT; 31 AA.  
ID Q9R4X1  
AC Q9R4X1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
ET 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
ET 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Hetelysin (Fragment).  
OS Treponema denticola.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=158;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94376628; PubMed=8090078;  
RA Chu L., Holt S.C.;  
RT "Purification and characterization of a 45 kDa hemolysin from  
RT Treponema denticola ATCC 35404.";  
RL Microb. Pathog. 16:197-212(1994).  
SQ SEQUENCE 31 AA; 3650 MW; 054650359C8F24C4 CRC64;

Query Match 84.8%; Score 28; DB 2; Length 31;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|||  
Db 5 FTLKISR 11

RESULT 15

Q9FAA7 PRELIMINARY; PRT; 80 AA.  
ID Q9FAA7  
AC Q9FAA7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Atpl protein.  
GN ATPI.  
OS Brevibacterium flavum.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=92706;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC14067;  
RA Sekine H., Tomita F., Yokota A.;  
RT "Nucleotide sequence of atp operon of Brevibacterium flavum.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB048368; BAB13353.1;  
SQ SEQUENCE 80 AA; 9339 MW; 72CD0E33367E4B33 CRC64;

Query Match 84.8%; Score 28; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKIS 6  
|||||  
Db 36 FTLKIS 41

Search completed: October 4, 2003, 12:25:19  
Job time : 51.6667 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:26 ; Search time 60.3333 Seconds  
(without alignments)  
18.416 Million cell updates/sec

Title: US-09-712-819C-6  
Perfect score: 33  
Sequence: 1 FLXISR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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20:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Length DB ID Description
1	33	100.0	32 19 AAW79207 Framework 3 region
2	33	100.0	32 22 AAB86295 Murine derived ant
3	33	100.0	32 23 ABP62672 Human immunopeptid
4	33	100.0	32 23 ABP62674 Human immunopeptid
5	33	100.0	32 23 AAJ70400 Human light chain
6	33	100.0	32 23 AAJ70440 Mouse light chain
7	33	100.0	50 23 ABG30477 Human anti-CD40 mo
8	33	100.0	50 23 ABG30478 Human anti-CD40 mo
9	33	100.0	50 23 ABG30479 Human anti-CD40 mo

10	33	100.0	81 17 AAR92994 Homologous sequenc
11	33	100.0	89 16 AAR83082 Mouse derived ligh
12	33	100.0	92 13 AAR27009 Hypercalcaemia age
13	33	100.0	93 21 AAY56670 Partial peptide fr
14	33	100.0	100 16 AAR72067 Of7K.7 VK-2 L chai
15	33	100.0	100 16 AAR72066 VK005 VK region.
16	33	100.0	100 22 AAEL2711 Antibody variable
17	33	100.0	100 22 AAEC6958 Murine iD9 antibod
18	33	100.0	100 22 AAEC6959 Youse germline kap
19	33	100.0	100 22 AAEC6960 Mouse germline kap
20	33	100.0	100 22 AAEC6961 Mouse germline kap
21	33	100.0	100 22 AAEC6962 Mouse germline kap
22	33	100.0	100 22 AAEC6963 Mouse germline kap
23	33	100.0	100 22 AAEC6964 Mouse germline kap
24	33	100.0	100 22 AAEC6965 Mouse germline kap
25	33	100.0	100 22 AAEC6966 Mouse germline kap
26	33	100.0	100 22 AAEC6967 Mouse germline kap
27	33	100.0	100 23 ABG76927 Humanised antibody
28	33	100.0	100 24 ABU58833 Mucin 1 (MUC-1) bi
29	33	100.0	100 24 ABJ18695 Antibody library r
30	33	100.0	101 14 AAR36529 Light chain variab
31	33	100.0	104 18 AAW04600 Anti-DNA antibody
32	33	100.0	104 24 ABG71455 Human monoclonal a
33	33	100.0	106 22 ABG58867 Human liver peptid
34	33	100.0	106 22 ABB43489 Peptide #10995 enc
35	33	100.0	106 22 ABB26451 Protein #8450 enco
36	33	100.0	106 22 AAM64423 Human brain expres
37	33	100.0	106 22 AAM77235 Human bone marrow
38	33	100.0	106 22 AAM21171 Peptide #7605 enco
39	33	100.0	106 22 AAM37382 Peptide #11419 enco
40	33	100.0	106 23 ABG46247 Human peptide enco
41	33	100.0	108 14 AAR38594 Human lambda light
42	33	100.0	108 19 AAW58494 Human kappa light
43	33	100.0	109 20 AAY39809 TR1.6 antibody lig
44	33	100.0	109 23 ABP52313 Fv region SC100 an
45	33	100.0	109 23 ABP52311 Fv region SC100 an

ALIGNMENTS

RESULT 1  
AAW79207  
ID AAW79207 standard; Protein: 32 AA.  
XX  
AC AAW79207;  
XX 21-DEC-1998 (first entry)  
XX Framework 3 region of human V kappa gene HUM5400.  
DE Monoclonal antibody; MAB; LO-CD2a; humanised antibody; CD2 antigen;  
XX human lymphocyte; immune response; chimeric; graft-versus-host disease;  
KW T-cell; transplant rejection; autoimmune disease; HUM5400.  
XX  
OS Homo sapiens.  
XX US5817311-A.  
XX  
XX 06-OCT-1998.  
XX  
XX 07-JUN-1995; 95US-0472281.  
XX  
XX 07-JUN-1995; 95US-0472281.  
XX 05-MAR-1993; 93US-0027008.  
XX 09-SEP-1993; 93US-0119032.  
XX 29-MAR-1995; 95US-0407009.  
XX  
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.  
XX  
XX Bazin H, Latinne D;  
XX WPI; 1998-556337/47.  
DR

```
XX Inhibition of T-cell mediated immune response with anti-CD2
PT monoclonal antibody LO-CD2a - used for preventing transplant
PT rejection or for treating graft-versus-host disease or auto-immune
PT diseases
XX Example 7; Columns 33-34; 96pp; English.
PS
XX This represents the amino acid sequence of the framework 3 region of
CC human V kappa gene HUM5400. This is used to construct a humanised antibody
CC LO-CD2a. The invention relates to the use of the monoclonal antibody
CC (MAB) LO-CD2a or a humanised or a chimeric version of the LO-CD2a
CC antibody for the inhibition of a T-cell mediated immune response in a
CC patient. The MAB LO-CD2a (produced by hybridoma cell line ATCC HB 1-123)
CC can bind to an epitope on the CD2 antigen of the human lymphocytes. The
CC T-cell mediated immune response in a patient can be inhibited by
CC administering the MAB LO-CD2a or an antibody that binds to the same
CC human lymphocyte epitope as LO-CD2a. The method is used for preventing
CC transplant rejection or for treating graft-versus-host disease or for
CC treating autoimmune diseases.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 19; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21
|||||

RESULT 2
AAB86295
ID AAB86295 standard; peptide; 32 AA.
XX
AC AAB86295;
XX
DT 13-SEP-2001 (first entry)
XX
DE Murine derived antibody Wue-1 light chain variable region FW-3.
XX
KW Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
KW immunomodulatory; cognate antigen identification; autoimmune disease;
KW tumor; multiple myeloma; lymphoma; plasmacytoma; FW-3.
XX
OS Mus sp.
XX
PN DE19962583-A1.
XX
PD 28-JUN-2001.
XX
PF 23-DEC-1999; 99DE-1062583.
XX
PR 23-DEC-1999; 99DE-1062583.
XX
PA (MUELLER) MUELLER-HERMELINK H K.
PA (GREINER) GREINER A.
XX
PI Mueller-Hermelink HK, Greiner A;
XX
DR WPI; 2001-426596/46.
XX
PT New antibodies specific for plasma cells, useful for treatment and
PT diagnosis of autoimmune diseases and plasma cell tumors.
XX
PS Claim 1; Page 10; 18pp; German.
XX
CC This invention describes novel antibodies (Ab) in which the variable
CC region (VR) of at least one chain and/or the VR of at least one heavy
CC chain includes at least one of 7 specified sequences, or fragments of
CC these sequences, or contain at least one light chain and/or heavy
CC chain encoded by specific nucleic acid sequences (I) and (II),

XX Inhibition of T-cell mediated immune response with anti-CD2
CC antitumor and immunomodulatory activity. Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursor stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional
CC chemotherapeutic agents. This sequence represents the Wue-1 antibody
CC variable region light chain FW-3 fragment described in the method of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21
|||||

RESULT 3
ABP62672
ID ABP62672 standard; Peptide; 32 AA.
XX
AC ABP62672;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein framework sequence #180.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US02303.
XX
PR 26-JAN-2001; 2001US-264451P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IV, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain
PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
PT (HCV), for diagnosing or treating patients having or suspected of
PT having HCV infection.
XX
PS Claim 4; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection.
XX
SQ Sequence 32 AA;
```

Query Match 100.0%; Score 33; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 4  
ABP62674  
ID ABP62674 standard; Peptide; 32 AA.

XX AC ABP62674;  
XX DT 10-OCT-2002 (first entry)  
XX DE Human immunopeptide to HCV E2 glycoprotein framework sequence #182.  
XX KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
XX QW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
XX NS3 protein; viral infection.

OS Homo sapiens.  
XX WO200259340-A1.  
XX PD 01-AUG-2002.  
XX PF 25-JAN-2002; 2002WO-US02303.  
XX PR 26-JAN-2001; 2001US-264451P.  
XX PA (SCRI) SCRIPPS RES INST.  
XX PI Maruyama T, Jones JM, Burton DR, Fox RI;  
XX WPI; 2002-599801/64.  
XX New human immunopolypeptide with binding specificity for certain  
PT envelope glycoproteins and nonstructural proteins of hepatitis C virus  
PT (HCV), for diagnosing or treating patients having or suspected of  
PT having HCV infection.

XX Claim 4; Fig 17; 308pp; English.  
XX The present invention relates to human immunopolypeptides, produced by a  
CC phage transfected cell library. The present sequence is one such  
CC immunopolypeptide. The immunopolypeptides have binding specificity for  
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
CC cell binding and contains neutralising epitopes, while NS3 is thought to  
CC be involved in the replication of HCV. The immunopolypeptides are useful  
CC for diagnosing and treating a patient having or suspected to be having  
CC HCV infection.

XX SQ Sequence 32 AA;  
Query Match 100.0%; Score 33; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 5  
AAU70400  
ID AAU70400 standard; Peptide; 32 AA.

XX AC AAU70400;

XX 14-FEB-2002 (first entry)  
XX DE Human light chain immunoglobulin framework region 3 #2.

XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array;  
KW IGM; IGG; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHSP.

OS Homo sapiens.  
XX WO200183806-A1.  
XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14349.  
XX PR 02-MAY-2000; 2000US-0563222.  
XX (EPIC-) EPICYTE PHARM INC.

XX HIATT AC, HEIN MB;  
XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.

XX Disclosure; Fig 1A; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that  
CC binds to a ligand, and transformed plant cells are selected, and  
CC preparing an IgBP array in plant cells. At least one peptide sequence has  
CC at least 75% sequence identity to a framework region (FR) of a native  
CC IGM, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.  
CC The method is useful for preparing an immunoglobulin binding protein  
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
CC desired characteristics. The present sequence is a mammalian  
CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
CC the invention.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 6  
AAU70440  
ID AAU70440 standard; Peptide; 32 AA.

XX AC AAU70440;

XX DT 14-FEB-2002 (first entry)

XX DE Mouse light chain immunoglobulin framework region 3 #2.

XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;

KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array;  
KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX Mus musculus.

XX WO2002:83806-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14349.

XX 02-MAY-2000; 2000US-0563222.

XX (EPIC-) EPICYTE PHARM INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array -

PS Disclosure; Fig 1A; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that  
CC binds to a ligand, and transformed plant cells are selected, and  
CC preparing an IgBP array in plant cells. At least one peptide sequence has  
CC at least 75% sequence identity to a framework region (FR) of a native  
CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.  
CC The method is useful for preparing an immunoglobulin binding protein  
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize;  
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
CC desired characteristics. The present sequence is a mammalian  
CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
CC the invention.

XX SQ Sequence 32 AA;  
Query Match 100.0%; Score 33; DB 23; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 7  
ABG30477  
ID ABG30477 standard; Protein; 50 AA.  
XX  
AC ABG30477;

XX 07-OCT-2002 (first entry)

DE Human anti-CD40 monoclonal antibody 5H7 light chain #2.

XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;  
KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;  
KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;  
KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;  
KW proliferation.

XX Homo sapiens.

XX WO200228904-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30857.

XX 02-OCT-2000; 2000US-237556P.

XX (CHIR) CHIRON CORP.

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;

XX WPI; 2002-402142/43.

XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting  
PT proliferation, growth or differentiation of a normal human B cells and  
PT treating autoimmune disease such as rheumatoid arthritis or systemic  
PT lupus erythematosus -

XX Claim 1; Fig 5; 75pp; English.

XX The invention relates to a human monoclonal antibody or fragment capable  
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed  
CC on the surface of human B cells), where the antibody or fragment is free  
CC of significant agonistic activity when it binds to the CD40 antigen, and  
CC the growth or differentiation is inhibited. The fragments comprise  
CC the complementarity determining region (CDR) of the light and heavy  
CC chains of the monoclonal antibodies secreted by a hybridoma consisting of  
CC 1538, 2004, 12D9, 9F7 and 13E4. Also included are the nucleic acids  
CC encoding the antibody (or fragments). The antibodies or fragments  
CC are used for inhibiting proliferation, growth or differentiation of a  
CC normal human B cells and to inhibit antibody production by B cells.  
CC They may also be useful for treating autoimmune diseases, such as  
CC systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory  
CC bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma  
CC (especially Non-Hodgkin's lymphoma). The present sequence represents  
CC the antibody 5H7 (another anti-CD40 antibody) light chain.

XX SQ Sequence 50 AA;

Query Match 100.0%; Score 33; DB 23; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 8  
ABG30478  
ID ABG30478 standard; Protein; 50 AA.  
XX  
AC ABG30478;

XX 07-OCT-2002 (first entry)

DE Human anti-CD40 monoclonal antibody 9F7 light chain #2.

XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;  
KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;  
KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;  
KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;  
KW proliferation.

XX Homo sapiens.

XX WO200228904-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30857.

XX 02-OCT-2000; 2000US-237556P.  
PR (CHIR ) CHIRON CORP.  
XX Chu K, Wang C, Yoshihara C, Donnelly JJ;  
XX WPI; 2002-402142/43.  
XX  
XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting  
PT proliferation, growth or differentiation of a normal human B cells and  
PT treating autoimmune disease such as rheumatoid arthritis or systemic  
PT lupus erythematosus -  
XX  
XX Claim 1; Fig 5; 75pp; English.  
XX  
XX The invention relates to a human monoclonal antibody or fragment capable  
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed  
CC on the surface of human B cells), where the antibody or fragment is free  
CC of significant agonistic activity when it binds to the CD40 antigen, and  
CC the growth or differentiation is inhibited. The fragments comprise  
CC the complementarity determining region (CDR) of the light and heavy  
CC chains of the monoclonal antibodies secreted by a hybridoma consisting of  
CC 15B8, 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids  
CC encoding the antibody (or fragments). The antibodies or fragments  
CC are used for inhibiting proliferation, growth or differentiation of a  
CC normal human B cells and to inhibit antibody production by B cells.  
CC They may also be useful for treating autoimmune diseases, such as  
CC systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory  
CC bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma  
CC (especially Non-Hodgkin's Lymphoma). The present sequence represents  
CC the antibody 9F7 light chain.  
XX  
SQ Sequence 50 AA;  
Query Match 100.0%; Score 33; DB 23; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2Y 1 FTLKISR 7  
15 FTLKISR 21  
Db  
RESULT 9  
ABG30479  
ID ABG30479 standard; Protein; 50 AA.  
XX  
AC ABG30479;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human anti-CD40 monoclonal antibody 15B8 light chain #2.  
XX  
KW Human; light chain; CD40; autoimmune disease; multiple sclerosis;  
KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;  
KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;  
KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;  
KW proliferation.  
XX  
DS Homo sapiens.  
XX  
SN WO200228904-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 02-OCT-2001; 2001WO-US30857.  
XX  
PR 02-OCT-2000; 2000US-237556P.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Chu K, Wang C, Yoshihara C, Donnelly JJ;

XX WPI; 2002-402142/43.  
XX  
XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting  
PT proliferation, growth or differentiation of a normal human B cells and  
PT treating autoimmune disease such as rheumatoid arthritis or systemic  
PT lupus erythematosus -  
XX  
XX Claim 1; Fig 5; 75pp; English.  
XX  
XX The invention relates to a human monoclonal antibody or fragment capable  
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed  
CC on the surface of human B cells), where the antibody or fragment is free  
CC of significant agonistic activity when it binds to the CD40 antigen, and  
CC the growth or differentiation is inhibited. The fragments comprise  
CC the complementarity determining region (CDR) of the light and heavy  
CC chains of the monoclonal antibodies secreted by a hybridoma consisting of  
CC 15B8, 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids  
CC encoding the antibody (or fragments). The antibodies or fragments  
CC are used for inhibiting proliferation, growth or differentiation of a  
CC normal human B cells and to inhibit antibody production by B cells.  
CC They may also be useful for treating autoimmune diseases, such as  
CC systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory  
CC bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma  
CC (especially Non-Hodgkin's Lymphoma). The present sequence represents  
CC the antibody 15B8 light chain.  
XX  
SQ Sequence 50 AA;  
Query Match 100.0%; Score 33; DB 23; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 FTLKISR 7  
15 FTLKISR 21  
Db  
RESULT 10  
AAR92994  
ID AAR92994 standard; Protein; 81 AA.  
XX  
AC AAR92994;  
XX  
DT 25-MAR-2003 (updated)  
DT 18-MAY-1996 (first entry)  
XX  
DE Homologous sequences to antibody ICR-R3 variable region light chain.  
XX  
KW ICR-R3; monoclonal antibody; human; mouse; light chain; homology;  
KW variable region; epidermal growth factor receptor; hybridoma;  
KW framework; cloning; computer; algorithm; immunogenicity;  
KW site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;  
KW point mutation; antibody engineering; protein engineering;  
KW humanised antibody; antitumour; cancer; therapy.  
XX  
OS Homo sapiens.  
XX  
PH Key  
FT Region 2 Location/Qualifiers  
FT /note= "Amino acid involved in tertiary structure"  
FT Region 4  
FT /note= "Amino acid involved in tertiary structure"  
FT Region 24..25  
FT /note= "Amino acids involved in tertiary structure"  
FT Region 35..39  
FT /note= "Amino acids involved in tertiary structure"  
FT Region 46  
FT /note= "Amino acid involved in tertiary structure"  
FT Region 48  
FT /note= "Amino acid involved in tertiary structure"  
FT Region 50..51  
FT /note= "Amino acids involved in tertiary structure"

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Region          53
/note= "Amino acid involved in tertiary structure"
FT
Region          71
/note= "Amino acid involved in tertiary structure"
FT
XX
EP699755-A2.
PN
XX
06-MAR-1996.
PD
XX
27-JUN-1995;   95EP-0201752.
PF
XX
30-JUN-1994;   94CU-CC0008C.
PR
XX
(IMMU-) CENT IMMUNOLOGY MOLECULAR.
PA
XX
Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
PI
WPI; :1996-130770/14.
DR
XX
Identifying interspecies differences in amino acid sequence of Ig
T-cell epitopes - by sequence comparison, also humanised antibodies
contg. altered T-cell epitopes, retaining antigen specificity but
not immunogenicity, esp. for tumour treatment
PT
XX
Claim 14; Fig 3; 33pp; English.
PS
XX
The sequence represents residues from a human immunoglobulin with
homology to the light chain variable region from monoclonal antibody
IOR-R3 (AAR92993), specific for epidermal growth factor receptor,
produced by a mouse hybridoma. The sequence is partial, and
complementarity determining regions are omitted. The sequence is
isolated by comparison of human and mouse immunoglobulins and
analysis for T-lymphocyte antigenic sequences using a computer
algorithm. Residues not within a complementarity determining region,
canonical structure or Vernier zone may be modified to reduce
immunogenicity in humans (e.g. in sequence AAR92995). This method,
which involves the introduction of only a few point mutations into
T-cell epitope coding regions, is generally applicable in humanisation
of mouse antibodies. The resulting humanised antibodies may be used
e.g. as antitumour agents. They retain the antigen recognition of the
original antibody, but are not immunogenic in humans.
CC
(Updated on 25-MAR-2003 to correct PI field.)
XX
SQ
Sequence      81 AA;

Query Match      100.0%; Score 33; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches       7; Conservative    0; Mismatches     0; Indels     0; Gaps

QY      1 FTLKISR 7
Db      53 FTLKISR 59
        |||||

RESULT 11
AAR80082
ID      AAR80082 standard; Protein; E9 AA.
XX
AC      AAR80082;
XX
DE      22-MAY-1996 (first entry)
XX
Mouse derived light chain RT3 phage antibody pattern I.
XX
Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW      pattern I.
XX
Mus musculus.
OS
XX
Key Location/Qualifiers
FH Region .:.14
FT /note= "framework region 1"
FT Region :5..28

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FT      /note= "complementarity determining region 1"
FT 29..42
FT      /note= "framework region 2"
FT 43..49
FT      /note= "complementarity determining region 2"
FT 50..82
FT      /note= "framework region 3"
FT 83..89
FT      /note= "complementarity determining region 3
FT      N-terminal fragment"
XX
XX WO9527045-A1.
XX
XX 12-OCT-1995.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX 30-MAR-1994; 94WO-US03420.
XX
XX (IGEN-) IGEN INC.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
XX Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
XX WPI; 1995-358624/46.
XX N-PSDB; AAT04629.
XX
XX Production of catalytic antibodies displayed on phage by
XX generating a gene library of antibody-derived domains and expressing
XX it in phage vectors
XX
XX Disclosure; Fig 10; 133pp; English.
XX
XX AAT04629 encodes AAR80082 mouse derived light chain RT3 phage antibody.
XX The DNA was used in the prepn. of catalytic antibody (CA) producing
XX bacteriophage. The CAs can be used to activate/deactivate a
XX biological function in an animal by enhancing the rate of cleavage,
XX or formation of a specific bond within a mol. in vivo.
XX
XX Sequence 89 AA;
XX
XX Query Match: 100.0%; Score 33; DB 16; Length 89;
XX Best Local Similarity 100.0%; Pred. No. 5.2;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
XX
XX QY 1 FTLKISR 7
XX |||||
XX 65 FTLKISR 71
XX
XX RESULT 12
XX AAR27009
XX ID AAR27009 standard; peptide; 92 AA.
XX
XX AC AAR27009;
XX
XX DT 20-MAY-1998 (first entry)
XX
XX DE Hypercalcaemia agent portion 2.
XX
XX KW Antihuman parathyroid hormone-related protein; monoclonal antibody;
XX variable region; rodent/human chimeric MAh; constant region; FTHR2.
XX
XX OS Synthetic.
XX
XX PN JP04228069-A.
XX
XX PD 18-AUG-1992.
XX
XX PF 15-MAY-1991; 91JP-C1:0565.
XX
XX PR 15-MAY-1990; 90JP-C124581.
XX

```

PA (KANF ) KANEXA CORP.  
XX  
DR WPI; 1992-320987/39.  
XX  
PT Treatment and preventive agent for hypercalcaemia - contg. one of  
PT anti-human para-thyroid-hormone-related protein monoclonal antibody,  
PT a rodent or chimera monoclonal antibody, fused gene and cell  
PT line, etc.  
XX  
PS Disclosure; Page 13; 18pp; Japanese.  
XX  
CC The sequences given in AAR27008-11 are fragments which were used in  
CC the construction of an agent for the treating and prevention of  
CC hypercalcaemia. The agent contained a portion of the anti-human  
CC parathyroid hormone-related protein monoclonal antibody (anti-human  
CC PTHrP MAb). The MAB was used as the active component in the agent.  
CC The agent further comprises a rodent/human chimeric MAB which has a  
CC rodent variable region and a human constant region and recognises  
CC human PTHrP.  
XX  
SQ Sequence 92 AA;  
Query Match 100.0%; Score 33; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 FTLKISR 7  
Db |||||  
68 FTLKISR 74  
RESULT 13  
ID AAY56670  
AC AAY56670; standard; protein; 93 AA.  
DT 25-FEB-2000 (first entry)  
DE Partial peptide fragment of Cynomolgus V kappa cDNA clone 4-5.  
CX Complementarity determining region; antibody; primate; immunogenicity;  
CW Old World ape; Old World monkey; antigen-binding affinity.  
XX  
CS Macaca cynomolgus.  
XX  
PN WO9955369-A1.  
XX  
PD 04-NOV-1999.  
XX  
PF 28-APR-1999; 99WO-US09131.  
XX  
PR 28-APR-1998; 98US-0083367.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Taylor AH;  
XX  
DR WPI; 2000-023265/02.  
DR N-PSDB; AAZ39338.  
XX  
PT Antibodies containing donor complementarity determining regions and  
PT non-human primate acceptor frameworks, having reduced immunogenicity in  
PT humans -  
XX  
PS Claim 26; Page 101; 123pp; English.  
XX  
CC The invention provides an antibody (Ab) comprising donor CDRs  
CC (complementarity determining regions) derived from a non-human antigen-  
CC specific donor antibody, and an acceptor framework from a non-human  
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-  
CC specific donor antibody onto homologous Old World ape or monkey acceptor  
CC frameworks. The Abs have reduced immunogenicity and are better tolerated

CC in humans (because of the close similarity between the human and primate  
CC proteins), but retain the full antigen-binding affinity of the donor  
CC antibody.  
XX  
SQ Sequence 93 AA;  
Query Match 100.0%; Score 33; DB 21; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 FTLKISR 7  
Db |||||  
76 FTLKISR 82  
RESULT 14  
ID AAR72067 standard; Protein; 100 AA.  
XX  
AC AAR72067;  
XX  
DT 25-MAR-2003 (updated)  
DT 26-SEP-1995 (first entry)  
XX  
DE OF7K.7 VK-2 L chain.  
XX  
KW Graves ophthalmopathy associated immunoglobulin protein;  
KW orbital antigen; monoclonal antibody; light chain; L chain;  
KW variable region; autoimmunity.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Region 23..38  
FT /label= CDR1  
FT Region 54..60  
FT /label= CDR2  
FT Region 93..100  
FT /label= CDR3  
XX  
PN WO9508336-A1.  
XX  
PD 30-MAR-1995.  
XX  
PF 22-SEP-1994; 94WO-US10756.  
XX  
PR 22-SEP-1993; 93US-0124469.  
XX  
PA (NICH-) NICHOLS INST DIAGNOSTICS.  
XX  
PI McLachlan SX, Rapoport B;  
XX  
DR WPI; 1995-139383/18.  
DR N-PSDB; AAQ89326.  
XX  
PT Graves' ophthalmopathy-associated monoclonal antibody - produced  
PT by molecular cloning of immunoglobulin genes by PCR  
XX  
PS Claim 4; Page 66; 94pp; English.  
XX  
CC L- and H-chain DNA was amplified by PCR from Graves' orbital  
CC tissue and clones encoding autoimmune-associated immunoglobulin  
CC fragments were obtained. 14/15 clones of L chain (kappa) regions  
CC showed homology to the putative VK germline gene KL012 (given in  
CC AAQ89317) and the remaining clone, OF7K.7 (AAQ89326), to the VK005  
CC gene.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 100 AA;  
Query Match 100.0%; Score 33; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 FTLKISR 7  
| | | | |  
Db 76 FTLKISR 82

RESULT 15  
AAR72066  
ID AAR72066 standard; Protein; 100 AA.  
XX AC AAR72066;  
XX DT 25-MAR-2003 (updated;  
DT 26-SEP-1995 (first entry)  
XX VK005 VK region.  
DE  
XX  
KW Graves ophthalmopathy associated immunoglobulin protein;  
KW orbital antigen; monoclonal antibody; light chain; L chain;  
KW variable region; autoimmunity.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FH Region 23..38  
FT /label= CDR1  
FT Region 54..60  
FT /label= CDR2  
FT Region 93..100  
FT /label= CDR3  
XX  
PN WO9508336-A1.  
XX  
PD 30-MAR-1995.  
XX  
PF 22-SEP-1994; 94WQ-US10756.  
XX  
PR 22-SEP-1993; 93US-0124469.  
XX  
PA (NICH-) NICHOLS INST DIAGNOSTICS.  
XX  
PI McLachlan SM, Rapoport B;  
XX  
DR WPI; 1995-139383/1a.  
DR N-PSDB; AAQ89325.  
XX  
PT Graves' ophthalmopathy-associated monoclonal antibody - produced  
PT by molecular cloning of immunoglobulin genes by PCR  
XX  
PS Disclosure; Page 67; 94pp; English.  
XX  
CC L- and H-chain DNA was amplified by PCR from Graves' orbital  
CC tissue and clones encoding autoimmune-associated immunoglobulin  
CC fragments were obtained. 14/15 clones of L chain (kappa) regions  
CC showed homology to the putative VK germline gene KLC12 (given in  
CC AAQ89317) and the remaining clone, OFK.7 (AAQ89326), to the VK005  
CC gene.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 100 AA;

Query Match 100.0%; Score 33; DB 16; Length 100;  
Best Local Similarity 100.0%; E-Val. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
| | | | |  
Db 76 FTLKISR 82

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:25:27 ; Search time 35.3333 Seconds  
(without alignments)  
31.344 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pcp.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09E\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US40\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US40\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	11	US-09-563-222-80 Sequence 80, Appl
2	33	100.0	32	11	US-09-563-222-120 Sequence 120, Appl
3	33	100.0	32	12	US-09-947-839-71 Sequence 71, Appl
4	33	100.0	32	12	US-10-168-809-5 Sequence 5, Appli
5	33	100.0	93	9	US-09-935-243-61 Sequence 61, Appl
6	33	100.0	99	12	US-10-041-860-281 Sequence 281, App
7	33	100.0	99	12	US-10-041-860-323 Sequence 323, App
8	33	100.0	99	12	US-10-041-860-365 Sequence 365, App
9	33	100.0	100	10	US-09-822-698A-19 Sequence 19, App-
10	33	100.0	100	10	US-09-840-459-21 Sequence 21, App-
11	33	100.0	100	10	US-09-840-459-22 Sequence 22, App-
12	33	100.0	100	10	US-09-840-459-23 Sequence 23, Appl
13	33	100.0	100	10	US-09-840-459-24 Sequence 24, Appl
14	33	100.0	100	10	US-09-840-459-25 Sequence 25, Appl
15	33	100.0	100	10	US-09-840-459-26 Sequence 26, Appl

16	33	100.0	100	10	US-09-840-459-27 Sequence 27, Appl
17	33	100.0	100	10	US-09-840-459-28 Sequence 28, Appl
18	33	100.0	100	10	US-09-840-459-29 Sequence 29, Appl
19	33	100.0	100	10	US-09-840-459-30 Sequence 30, Appl
20	33	100.0	100	12	US-10-041-860-8 Sequence 8, Appli
21	33	100.0	100	12	US-10-041-860-280 Sequence 280, App
22	33	100.0	100	12	US-10-041-860-321 Sequence 321, App
23	33	100.0	100	12	US-10-041-860-364 Sequence 364, App
24	33	100.0	100	12	US-10-010-942B-7 Sequence 7, Appli
25	33	100.0	100	14	US-13-025-687-24 Sequence 24, Appl
26	33	100.0	100	15	US-10-194-975-75 Sequence 75, App-
27	33	100.0	100	15	US-10-194-975-76 Sequence 76, Appl
28	33	100.0	100	15	US-10-194-975-77 Sequence 77, Appl
29	33	100.0	100	15	US-10-194-975-78 Sequence 78, Appl
30	33	100.0	100	15	US-10-194-975-79 Sequence 79, Appl
31	33	100.0	100	15	US-10-194-975-80 Sequence 80, Appl
32	33	100.0	100	15	US-10-194-975-81 Sequence 81, Appl
33	33	100.0	100	15	US-10-125-687-24 Sequence 24, Appl
34	33	100.0	100	15	US-10-153-382-36 Sequence 36, Appl
35	33	100.0	100	15	US-10-153-382-38 Sequence 38, Appl
36	33	100.0	101	11	US-09-972-656-131 Sequence 131, App
37	33	100.0	101	11	US-09-972-656-132 Sequence 132, App
38	33	100.0	101	15	US-10-194-975-73 Sequence 73, Appl
39	33	100.0	101	15	US-10-194-975-74 Sequence 74, Appl
40	33	100.0	106	9	US-09-864-761-41749 Sequence 41749, A
41	33	100.0	108	12	US-10-127-890-151 Sequence 151, App
42	33	100.0	110	9	US-09-864-761-48276 Sequence 48276, A
43	33	100.0	111	9	US-09-835-087-2 Sequence 2, Appli
44	33	100.0	111	20	US-09-839-739-13 Sequence 13, Appl
45	33	100.0	111	10	US-09-840-459-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-563-222-80  
; Sequence 80, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-563-222-80

Query Match 100.0%; Score 33; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 2  
US-09-563-222-120  
; Sequence 120, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hiatt, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS

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; SEQ ID NO 19
; LENGTH: 100
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region from a DPK 15 germ line
US-09-822-698A-19

Query Match.          100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
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Db 76 FTLKISR 82

RESULT 10
US-09-840-459-21
; Sequence 21, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-21

Query Match          100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
   |||||
Db 76 FTLKISR 82

RESULT 11
US-09-840-459-22
; Sequence 22, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
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; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-22

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Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
   |||||
Db 76 FTLKISR 82

RESULT 12
US-09-840-459-23
; Sequence 23, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-23

Query Match          100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
   |||||
Db 76 FTLKISR 82

RESULT 13
US-09-840-459-24
; Sequence 24, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
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APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(100)  
OTHER INFORMATION: Xaa = Any Amino Acid  
S-09-840-459-24

Query Match 100.0%; Score 33; DB 10; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 FTLKISR 7  
| | | | |  
b 76 FTLKISR 82

RESULT 14  
S-09-840-459-25  
Sequence 25, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 25  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
S-09-840-459-25

Query Match 100.0%; Score 33; DB 10; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTLKISR 7  
| | | | |  
Db 76 FTLKISR 82

RESULT 15  
US-09-840-459-26  
Sequence 26, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-840-459-26

Query Match 100.0%; Score 33; DB 10; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
| | | | |  
Db 76 FTLKISR 82

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:18:55 ; Search time 17.6667 Seconds  
(without alignments)  
16.765 Million cell updates/sec

Title: US-09-712-819C-6  
Perfect score: 33  
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	1	US-08-477-877B-33
2	33	100.0	32	1	US-07-977-696C-71
3	33	100.0	32	1	US-08-129-933E-71
4	33	100.0	32	2	US-08-472-281A-33
5	33	100.0	32	2	US-08-477-983R-33
6	33	100.0	32	4	US-08-976-288A-71
7	33	100.0	61	1	US-08-497-312-19
8	33	100.0	104	3	US-08-881-337-37
9	33	100.0	108	1	US-08-488-113B-151
10	33	100.0	108	1	US-08-477-484B-151
11	33	100.0	108	1	US-08-107-669D-15
12	33	100.0	108	1	US-08-472-788A-15
13	33	100.0	108	2	US-08-477-531B-15
14	33	100.0	108	2	US-08-646-360-151
15	33	100.0	108	2	US-08-082-842A-15
16	33	100.0	108	2	US-08-378-939-22
17	33	100.0	108	2	US-08-378-939-28
18	33	100.0	108	2	US-08-939-30
19	33	100.0	108	3	US-08-839-765-151
20	33	100.0	108	3	US-09-136-389-151
21	33	100.0	108	4	US-09-610-838-151
22	33	100.0	110	1	US-08-244-626-2
23	33	100.0	111	1	US-07-942-245-29
24	33	100.0	112	1	US-08-053-171-15
25	33	100.0	112	1	US-08-053-171-16
26	33	100.0	112	1	US-08-331-398A-48
27	33	100.0	112	1	US-08-331-398A-49

28	33	100.0	112	1	US-08-331-398A-50
29	33	100.0	112	1	US-07-942-245-28
30	33	100.0	112	1	US-08-478-039-88
31	33	100.0	112	1	US-08-478-039-89
32	33	100.0	112	1	US-08-477-877B-89
33	33	100.0	112	1	US-08-277-252B-3
34	33	100.0	112	1	US-08-476-349A-88
35	33	100.0	112	1	US-08-476-349A-89
36	33	100.0	112	1	US-08-388-672A-25
37	33	100.0	112	2	US-08-475-000-18
38	33	100.0	112	2	US-08-472-281A-59
39	33	100.0	112	2	US-08-483-199-18
40	33	100.0	112	2	US-08-859-649-19
41	33	100.0	112	2	US-08-859-649-29
42	33	100.0	112	2	US-08-606-293-4
43	33	100.0	112	2	US-08-606-293-8
44	33	100.0	112	2	US-08-678-194-6
45	33	100.0	112	2	US-08-752-844-15

ALIGNMENTS

RESULT 1  
US-08-477-877B-33  
; Sequence 33, Application.US/08477877B  
; Patent No. 5730979  
; GENERAL INFORMATION:  
; APPLICANT: Bazin, Herv  
; APPLICANT: Latinne, Dominique  
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Acti  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrre, Bair, Gilfillan,  
; ADDRESSEE: Cecchi, Stewart & Orstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IEX PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,877E  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/407,009  
; FILING DATE: 29-MAR-1995  
; APPLICATION NUMBER: 08/119,032  
; FILING DATE: 09-SEP-1993  
; APPLICATION NUMBER: 08/027,008  
; FILING DATE: 05-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliot M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 61750-146  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
US-08-477-877B-33

Query Match 100.0%; Score 33; DB 1; Length 32;

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2
US-07-977-696C-71
; Sequence 71, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPJAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 3
US-08-129-930B-71
; Sequence 71, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
```

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; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 4
US-08-472-281A-33
; Sequence 33, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
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APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 06/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

JS-08-472-281A-33

Query Match 100.0%; Score 33; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 FTLKISR 7

|||||

b 15 FTLKISR 21

RESULT 5

S-08-477-989B-33

Sequence 33, Application US/08477989B

Patent No. 5951983

GENERAL INFORMATION:

APPLICANT: Bazin, Herv

APPLICANT: Latinne, Dominique

APPLICANT: Kapiian, Ruth

APPLICANT: Kieber-Emmons, Thomas

APPLICANT: Postema, Christina E.

APPLICANT: White-Scharf, Mary

TITLE OF INVENTION: LC-CD2a Antibody and Uses

TITLE OF INVENTION: Thereof for Inhibiting

TITLE OF INVENTION: T-Cell Activation and

TITLE OF INVENTION: Proliferation

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byron, Bain, Gilfillan,

ADDRESSEE: Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,989B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407,009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119,032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027,008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24,025

REFERENCE/DOCKET NUMBER: 61750-147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

US-38-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7

|||||

DB 15 FTLKISR 21

RESULT 6

US-08-976-288A-71

Sequence 71, Application US/08976288A

Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder & Poplawski

STREET: 444 South Flower St., 19th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A

FILING DATE: No. 6315997ember 21, 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,950

FILING DATE: September 30, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,696

FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P6639938

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-976-288A-71

Query Match 100.0%; Score 33; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTLKISR 7  
Db 15 FTLKISR 21

RESULT 7  
US-08-497-312-19  
; Sequence 19, Application US/08497312  
; Patent No. 5712126  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method for obtaining modified  
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
; TITLE OF INVENTION: antibody variable domains, compositions containing them.  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
; STREET: 215 Y 15, ATABEY PLAYA  
; CITY: HAVANA  
; STATE:  
; COUNTRY: CUBA  
; ZIP: 11600  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO);  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/497,312  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CU 80/94  
; FILING DATE: 30-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BOND, LAURENCE B.  
; REGISTRATION NUMBER: 30,549  
; REFERENCE/DOCKET NUMBER: 2629US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 801/532-1922  
; TELEFAX: 801/531-9268  
; TELEX: 388961 LPM04UT  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 81 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-497-312-19

Query Match 100.0%; Score 33; DB 1; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
Db 53 FTLKISR 59

RESULT 8  
US-08-881-037-37  
; Sequence 37, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Konski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5630  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-37

Query Match 100.0%; Score 33; DB 3; Length 104;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
Db 68 FTLKISR 74

RESULT 9  
US-08-488-113B-151  
; Sequence 151, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:



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; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/757,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 1:022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
JS-08-488-113B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

>
> 1 FTLKISR 7
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> 72 FTLKISR 78

RESULT 10
IS-08-477-484B-151
Sequence 151, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroil, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 1:022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-477-484B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Qb |||||
Qb 72 FTLKISR 78

RESULT 11
US-08-107-669D-15
Sequence 15, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.C.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
```

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-15  
Query Match 100.0%; Score 33; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 72 FTLKISR 78

RESULT 12  
US-08-472-788A-15  
Sequence 15, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000033  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-788A-15

Query Match 100.0%; Score 33; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 72 FTLKISR 78

RESULT 13

US-08-477-531B-15  
Sequence 15, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-531B-15  
Query Match 100.0%; Score 33; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
Db 72 FTLKISR 78  
RESULT 14  
US-08-646-360-15  
Sequence 15, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
3-08-646-360-15:

Query Match: 100.0%; Score 33; DB 2; Length 108;  
Best Local Similarity: 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FTLKISR 7  
72 FTLKISR 78

RESULT 15  
3-08-082-842A-15  
Sequence 15, Application: US/08082842A  
Patent No. 5869619  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,842A  
FILING DATE: 23-JUN-1993

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cirbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-082-842A-15  
Query Match: 100.0%; Score 33; DB 2; Length 108;  
Best Local Similarity: 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7  
Db 72 FTLKISR 78

Search completed: October 4, 2003, 12:27:23  
Job time: 18.6667 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:52 ; Search time 19.3333 Seconds  
(without alignments)  
34.920 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	34.4	4	A40135	branched-chain-ami
2	11	34.4	5	PT0644	T-cell receptor be
3	11	34.4	5	B44817	34.5K structural p
4	11	34.4	5	D44817	35K structural pro
5	10	31.2	7	E30608	Ig kappa chain V-I
6	9	28.1	3	T13892	Cytochrome-c oxida
7	9	28.1	5	E42364	flagellar protein
8	9	28.1	5	E60274	major protein anti
9	9	28.1	5	A37114	hypoxanthine phosph
10	9	28.1	5	H44817	34.5K structural p
11	9	28.1	5	F44817	34.5K structural p
12	9	28.1	5	S69237	surface protein co
13	9	28.1	6	A60986	N-formyl oligopept
14	9	28.1	6	S14153	paraspinal crystal
15	9	28.1	6	A43766	28K ubiquitin immu
16	9	28.1	6	I37263	Y protein - human
17	9	28.1	6	I65546	MHC H2-D antigen -
18	9	28.1	7	S25266	pile protein - Esc
19	9	28.1	7	A25269	sex pheromone cAMP
20	9	28.1	7	A30812	sex pheromone cCF1
21	9	28.1	7	PS0254	18K protein 5537 -
22	9	28.1	7	PN0649	puilulanase (EC 3.
23	9	28.1	7	S09066	globulin IV alpha
24	8	25.0	3	PT0622	T-cell receptor be
25	8	25.0	4	PT0696	T-cell receptor be
26	8	25.0	4	PT0645	T-cell receptor be
27	8	25.0	4	PT0712	T-cell receptor be
28	8	25.0	4	PT0698	T-cell receptor be
29	8	25.0	4	PT0551	T-cell receptor be

30	8	25.0	4	2	PT0697	T-cell receptor be
31	8	25.0	5	2	A60521	Glycogen phosphory
32	8	25.0	5	2	I40698	biotin B - Citroba
33	8	25.0	5	2	I39964	ribosomal protein
34	8	25.0	5	2	I39966	ribosomal protein
35	8	25.0	5	2	I39965	ribosomal protein
36	8	25.0	5	2	T10954	hypothetical prote
37	8	25.0	5	2	I50385	myosin light chain
38	8	25.0	5	2	PT0308	Ig heavy chain CRD
39	9	25.0	5	2	PT0596	T-cell receptor be
40	9	25.0	5	2	PT0610	T-cell receptor be
41	9	25.0	5	2	PT0597	T-cell receptor be
42	8	25.0	5	2	PT0600	T-cell receptor be
43	8	25.0	5	2	PT0729	T-cell receptor be
44	8	25.0	5	2	PT0624	T-cell receptor be
45	8	25.0	5	2	PT0686	T-cell receptor be

ALIGNMENTS

RESULT 1

A40135  
branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)  
N: Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial  
C: Species: Rattus norvegicus (Norway rat)  
C: Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 30-Sep-1993  
C: Accession: A40135  
R: Hutson, S.M.; Wallin, R.; Hall, T.R.  
Submitted to the Protein Sequence Database, March 1992  
A: Reference number: A40135  
A: Accession: A40135  
A: Status: preliminary  
A: Molecule type: protein  
A: Residues: 1-4 <HUT>  
C: Keywords: aminotransferase; mitochondrion

Query Match 34.4%; Score 11; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7  
||  
LB 1 VSS 3

RESULT 2

PT0644  
T-cell receptor beta chain V-D-J region (111-16) - mouse (fragment)  
C: Species: Mus musculus (house mouse)  
C: Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C: Accession: PT0644  
R: Feeney, A.J.  
C: Exp. Med. 174, 115-124, 1991  
A: Title: Functional sequences of fetal T cell receptor beta chains have few N regions  
A: Reference number: PT0509; MUID:91277601; PMID:1711558  
A: Accession: PT0644  
A: Status: translation not shown  
A: Molecule type: mRNA  
A: Residues: 1-5 <FEE>  
A: Experimental source: newborn thymus, strain BALB/c  
C: Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
||  
DB 4 FT 5

RESULT 3

B44817  
 34.5K structural protein - Leuconostoc oenos phage P2c11-15 (fragment)  
 C/Species: Leuconostoc oenos phage P2c11-15  
 C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C/Accession: B44817  
 R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A/Title: Lysogeny in Leuconostoc oenos.  
 A/Reference number: A44817; MUID:92085033; PMID:1748869  
 A/Accession: B44817  
 A/Molecule type: protein  
 A/Residues: 1-5 <ARE>  
 A/Note: sequence extracted from NCBI backbone (NC51P:70342)

Query Match 34.4%; Score 11; DB 2; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTSS 7  
 | | |  
 Db 1 LATSS 5

RESULT 4  
 B44817  
 35K structural protein - Leuconostoc oenos phage P2c11-15 (fragment)  
 C/Species: Leuconostoc oenos phage P2c11-15  
 C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C/Accession: B44817  
 R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A/Title: Lysogeny in Leuconostoc oenos.  
 A/Reference number: A44817; MUID:92085033; PMID:1748869  
 A/Accession: B44817  
 A/Molecule type: protein  
 A/Residues: 1-5 <ARE>  
 A/Note: sequence extracted from NCBI backbone (NC51P:70342)

Query Match 34.4%; Score 11; DB 2; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTSS 7  
 | | |  
 Db 1 LATSS 5

RESULT 5  
 E30608  
 Ig kappa chain V-III region (Gag) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
 C/Accession: E30608  
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carlson, D.; Solidi, J.  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: E30608  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-7 <GCN>  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 31.2%; Score 10; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTSS 6  
 | | |  
 Db 4 LTQS 7

RESULT 6  
 E30608  
 Ig kappa chain V-III region (Gag) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
 C/Accession: E30608  
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carlson, D.; Solidi, J.  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: E30608  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-7 <GCN>  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 31.2%; Score 10; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTSS 6  
 | | |  
 Db 4 LTQS 7

T13892  
 cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f  
 C/Species: Mitochondrion Lampetra fluviatilis (river lamprey)  
 C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C/Accession: T13892  
 R/Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
 Mol. Biol. Evol. 14, 807-813, 1997  
 A/Title: The main features of the craniate mitochondrial DNA between the ND1 and the  
 A/Reference number: Z17775; MUID:97398704; PMID:9254918  
 A/Accession: T13892  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-3 <DEL>  
 A/Cross-references: EMBL:Y09528; NID:G2340016; FID:CAA70721.1; PID:G4379123  
 C/Genetics:  
 A/Genome: mitochondrion  
 A/Note: COI  
 C/Keywords: mitochondrion; oxidoreductase

Query Match 28.1%; Score 9; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
 | |  
 Db 2 TL 3

RESULT 7  
 E42364  
 flagellar protein flir - Salmonella typhimurium (fragment)  
 C/Species: Salmonella typhimurium  
 C/Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
 C/Accession: E42364  
 R/Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
 J. Bacteriol. 173, 3564-3572, 1991  
 A/Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and  
 A/Reference number: A42364; MUID:91258342; PMID:1646201  
 A/Accession: E42364  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-5 <VOG>  
 A/Cross-references: GB:M62408

Query Match 28.1%; Score 9; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
 | |  
 Db 3 TL 4

RESULT 8  
 E60274  
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C/Accession: E60274  
 R/Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, N.  
 Infect. Immun. 59, 372-382, 1991  
 A/Title: Isolation and partial characterization of major protein antigens in the cult  
 A/Reference number: A60274; MUID:91099389; PMID:1898899  
 A/Accession: E60274  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLT 4

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Db          2 YFIT 5
          : ||
          : ||

RESULT 9
A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm
C;Species: Schistosoma mansoni
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C;Accession: A37114
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Fur
A;Reference number: A37114; MUID:90337955; PMID:2199439
A;Accession: A37114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <YUA>
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match      28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          5 ISS 7
          : ||
          : ||
          : MSS 3

Db          1 MSS 3
          : ||
          : ||

RESULT 10
H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C;Species: Leuconostoc oenos phage P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: H44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: H44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBI:P:70332)

Query Match      28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY          3 LTSS 7
          : ||
          : ||
          : MATSS 5

Db          1 MATSS 5
          : ||
          : ||

RESULT 11
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C;Species: Leuconostoc oenos phage P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: F44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBI:P:70335)

Query Match      28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY          3 LTSS 7
          : ||
          : ||
          : MATSS 5

Db          1 MATSS 5
          : ||
          : ||

RESULT 12
S69237
surface protein tetraabrachion heavy chain - Staphylococcus marinus (fragment)
C;Species: Staphylococcus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
R;Peters, J.; Nitsch, M.; Kuehlmergen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engel
J. Mol. Biol. 245, 385-401, 1995
A;Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of unu
A;Reference number: S69237; MUID:95139068; PMID:7837271
A;Accession: S69237
A;Molecule type: protein
A;Residues: 1-5 <PET>
A;Experimental source: strain F1, DSM 3639
C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match      28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 TL 3
          : ||
          : ||
          : TL 3

Db          2 TL 3
          : ||
          : ||

RESULT 13
A60986
N-formyl oligopeptide - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A60986
R;Brook, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methi
A;Reference number: A60986; MUID:90392408; PMID:2689204
A;Accession: A60986
A;Molecule type: protein
A;Residues: 1-6 <BRO>
C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported
P;1/Modified site: N-formylmethionine #status experimental

Query Match      28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 FTL 3
          : ||
          : ||
          : FIL 5

Db          3 FIL 5
          : ||
          : ||

RESULT 14
S14159
parasporal crystal protein CryIC - Bacillus thuringiensis (fragment)
N;Alternate names: delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: S14159
R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
A;Title: Two structural domains as a general fold of the toxic fragment of the Bacilli
A;Reference number: S14087; MUID:91153300; PMID:1847865
A;Accession: S14159
A;Molecule type: protein
A;Residues: 1-6 <CON>

Query Match      28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 5 ISS 7  
Db 1 IST 3

RESULT 15

A43766  
28K ubiquitin-immunoreactive protein - inky cap (Coprinus cinereus) (fragment)  
C:Species: Coprinus cinereus  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 30-Sep-1993  
C:Accession: A43766  
R:Kanda, T.; Inoue, M.; Akiyama, M.  
Biochimie 72, 355-359, 1990  
A:Title: Purification and characterization of an ubiquitin-immuno-reactive protein local  
A:Reference numbers: A43766; PMID:9102724; PMID:1698461  
A:Accession: A43766  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <KAN>

Query Match 29.1% Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Prod. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TL 3  
Db 5 TL 6

Search completed: October 4, 2003, 12:49:36  
Job time : 21.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:27:32 ; Search time 10 Seconds  
(without alignments)  
32.919 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127853 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	37.5	7	1	P99025 mus musculus
2	11	34.4	5	1	RE31_LITRU
3	11	34.4	5	1	RE32_LITRU
4	10	31.2	5	1	E104_LITRU
5	9	28.1	7	1	CCP1_ENTFA
6	9	28.1	7	1	C1A_ENTFA
7	8	25.0	5	1	AL14_CARMA
8	8	25.0	5	1	B10B_CITFR
9	8	25.0	5	1	PSK_DAUCA
10	8	25.0	6	1	LOK1_LOCMI
11	8	25.0	7	1	ALJ2_CARMA
12	8	25.0	7	1	ALJ3_CARMA
13	8	25.0	7	1	ALJ4_CARMA
14	8	25.0	7	1	ALJ5_CARMA
15	8	25.0	7	1	ALJ7_CYOPO
16	8	25.0	7	1	UC24_MAIZE
17	7	21.9	4	1	E0S1_HUMAN
18	7	21.9	4	1	RM01_YEAS
19	7	21.9	5	1	B10A_CITFR
20	7	21.9	6	1	UN06_CLOPA
21	6	19.8	4	1	ACH1_ACHFU
22	6	19.8	4	1	PAR3_HIRME
23	6	18.8	4	1	PAR4_HIRME
24	6	18.8	4	1	PFKA_ATEL
25	6	18.8	4	1	FLRF_HIRME
26	6	18.8	4	1	FLRN_ATEL
27	6	18.8	4	1	PMRF_WACNU
28	6	18.8	4	1	FYRI_ATEL
29	6	18.8	4	1	CCP1_OCTM
30	6	18.8	5	1	E103_LITRU
31	6	18.8	5	1	FARP_ARTTR
32	6	18.8	5	1	PAP2_PARVA
33	6	18.8	5	1	RE11_LITRU

34	6	18.8	5	1	RE21_LITRU
35	6	18.8	5	1	SUGA_ACHFO
36	6	18.8	5	1	TPIS_CANFA
37	6	18.8	5	1	UC22_MAIZE
38	6	18.8	6	1	CIP1_MYTEB
39	6	18.8	6	1	CIP2_MYTEB
40	6	18.8	6	1	E101_LITRU
41	6	18.8	6	1	FARP_WONEX
42	6	18.8	7	1	FAR1_ASCSU
43	6	18.8	7	1	FAR1_HEGTT
44	6	18.8	7	1	FAR1_WACES
45	6	18.8	7	1	FAR1_PROCL

ALIGNMENTS

RESULT 1:  
GFRP\_MOUSE  
ID GFRP\_MOUSE STANDARD; PRT; 7 AA.  
AC P99025;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).  
GN GCHFR OR GFRP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,  
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
RA Cowthorne M.;  
RL Submitted (AJG-1998) to the SWISS-PROT data bank.  
CC - FUNCTION: MEDIATES TETRAHYDROBIPTERIN INHIBITION OF GTP  
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE  
(BY SIMILARITY).  
CC - SUBUNIT: Homodimer (By similarity).  
DR SWISS-2DPAGE; P99025; MOUSE.  
FT INIT MET 0  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 7;  
Best Local Similarity 60.0%; Pred. No. 13e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTISS 7  
DB 3 LLIST 7

RESULT 2  
RE31\_LITRU  
ID RE31\_LITRU STANDARD; PRT; 5 AA.  
AC P82072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;



RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=655; METHCD=FAR.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 5 5 AMIDATION.  
 SQ SEQUENCE 5 AA: 656 MW; 71A9C9CB1030030 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 ||  
 Db 4 FT 5

## RESULT 3

RE32\_LITRU  
 ID RE32\_LITRU STANDARD; PRT; 5 AA.  
 AC P82673;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litori electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 5 AA: 570 MW; 71A9C9CB2A00000 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 ||  
 Db 4 FT 5

## RESULT 4

E1C4\_LITRU  
 ID E1C4\_LITRU STANDARD; PRT; 5 AA.  
 AC P82100;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litori electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 5 5 AMIDATION.  
 SQ SEQUENCE 5 AA: 616 MW; 61F2D1A959A00000 CRC64;

Query Match 31.2%; Score 10; DB 1; Length 5;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTI 5  
 ||  
 Db 2 ITV 4

## RESULT 5

CCF1\_ENTFA  
 ID CCF1\_ENTFA STANDARD; PRT; 7 AA.  
 AC P20134;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CCF10.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8908313; PubMed=3136656;  
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
 RA Adsit J.C., Dunny G.M., Suzuki A.;  
 RT "Structure of CCF10, a peptide sex pheromone which induces  
 RT conjugative transfer of the Streptococcus faecalis tetracycline  
 RT resistance plasmid, pCF10."  
 RL J. Biol. Chem. 263:14574-14578(1988).  
 CC -1- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PCF10.  
 DR PIR; A30812; A30812.  
 KW Pheromone.  
 SQ SEQUENCE 7 AA: 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
 ||  
 Db 3 TL 4

## RESULT 6

C1A\_ENTFA  
 ID C1A\_ENTFA STANDARD; PRT; 7 AA.  
 AC P11932;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CAM373 (Clumping-inducing agent) (C1A).  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=87005252; PubMed=3093276;  
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,  
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the Streptococcus faecalis sex pheromone,  
 RL CAM373.";  
 RT FEBS Lett. 236:69-72(1988).  
 CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS  
 CC HARBORING PAM373.  
 CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR  
 CC SPECIFICITY OF PHEROMONES TO PLASMIDS.  
 CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.  
 DR PIR; A25269; A25269.  
 KW Pheromone.  
 SQ SEQUENCE 7 AA; 734 MW; 75BDD7259C05D80 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 |  
 |  
 DB 3 FIL 5

## RESULT 7

ALL4\_CARMA  
 ID ALL4\_CARMA STANDARD; PRT; 5 AA.

AC P818I7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostatin 14.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 CX NCBI\_TaxID=6759;  
 RN [1]

## SEQUENCE.

RP TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RC MEDLINE=98121193; PubMed=9461295;  
 RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW MOD RES 5  
 FT AMIDATION (POTENTIAL).  
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 |  
 |  
 DB 3 FGL 5

## RESULT 8

BIOB\_CITFR  
 ID BIOB\_CITFR STANDARD; PRT; 5 AA.

AC P12997;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).  
 GN BIOB.

OS Citrobacter freundii.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Citrobacter.  
 CX NCBI\_TaxID=546;  
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89006280; PubMed=2971595;  
 RA Shihua D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons.";  
 RL Gene 67:203-211(1988).  
 CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.  
 CC -!- PATHWAY: Biotin biosynthesis; last step.  
 CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES  
 CC FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
 DR EMBL; M21922; -; NOT\_ANNOTATED\_CDS.

DR PIR; I40698; I40698.

KW Biotin biosynthesis; Iron-sulfur; Transferase.

FT NON\_TER 5

SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SS 7  
 |  
 |  
 DB 4 SS 5

## RESULT 9

PSK\_DAJCA  
 ID PSK\_DAJCA STANDARD; PRT; 5 AA.

AC P58261;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].  
 OS Daucus carota (Carrot).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; campanulids; Apiales; Apiaceae; Daucus.  
 CX NCBI\_TaxID=4039;  
 RN [1]  
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
 RC STRAIN=cv. US-Harumakigoseun;  
 RX MEDLINE=20212743; PubMed=10750705;  
 RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,  
 RA Kamada H., Sakagami Y.;  
 RT "A secreted peptide growth factor, phytosulfokine, acting as a  
 RT stimulatory factor of carrot somatic embryo formation.";  
 RL Plant Cell Physiol. 41:27-32(2000).  
 CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
 CC EMBRYOS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
 CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
 KW Growth factor; Sulfation.  
 FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.  
 FT MOD\_RES 1 1 SULFATION.  
 FT MOD\_RES 3 3 SULFATION.  
 SQ SEQUENCE 5 AA; 687 MW; 76C1BB534B300000 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
!  
3 YT 4

Db RESULT 10  
LCK1\_LOCM1  
ID LCK1\_LOCM1 STANDARD; PRT; 6 AA.  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
CX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=22262851; PubMed=585017;  
RA Schoofs L., Holman G.M., Proost P., van Damme L., Hayes J.K.,  
de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
RT isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:49-57(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
CC of ion transport and inhibition of diuretic activity in Malpighian  
CC tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; A61069; A61068.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 654 MW; 586365A5E9CDB300 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SS 7  
!  
3 SS 4

RESULT 11  
ALL2\_CARMA  
ID ALL2\_CARMA STANDARD; PRT; 7 AA.  
AC P81805;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 2.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=99121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 770 MW; 672879CDB5DB70 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
!  
5 FGL 7

RESULT 12  
ALL3\_CARMA  
ID ALL3\_CARMA STANDARD; PRT; 7 AA.  
AC P81806;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 3.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 796 MW; 672879CDB476B70 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
!  
5 FGL 7

RESULT 13  
ALL4\_CARMA  
ID ALL4\_CARMA STANDARD; PRT; 7 AA.  
AC P81807;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 4.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 782 MW; 672879CDB476A00 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;

Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FTL 3  
DB 5 FGL 7

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FTL 3  
DB 5 FGL 7

Search completed: October 4, 2003, 12:46:00  
Job time : 12 secs

RESULT 14  
ALL5\_CARMA  
ID ALL5\_CARMA STANDARD; PRT; 7 AA.  
AC P81808;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 5.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubranchyura; Portunoidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
DB 5 FGL 7

RESULT 15  
ALL7\_CYPDPO  
ID ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiaastatin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=32600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.C., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 ; Search time 48 Seconds  
(without alignments)  
37,633 Million cell updates/sec

Title: US-09-712-819c-1

Perfect score: 32

Sequence: 1 FILTER 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	50.0	7	2	P70804
2	12	37.5	7	2	O34028
3	11	34.4	7	2	Q54248
4	9	28.1	7	2	O07354
5	9	28.1	7	10	P82445
6	9	28.1	7	15	O8JF81
7	8	25.0	6	10	P82181
8	8	25.0	6	10	P82182
9	8	25.0	7	2	P72081
10	7	21.9	7	2	Q47029
11	7	21.9	7	12	Q65578
12	6	18.8	5	13	P83308
13	6	18.8	6	10	P82541
14	6	18.8	7	2	O50556
15	6	18.8	7	2	O8KMS9
16	6	18.8	7	4	Q15903

O98866 spinacia ol  
O95945 saccharomyc  
O9C5B3 arabidopsis  
O8K3H6 rattus norv  
O9YGL3 transmissib  
C42564 fugu rubrip  
P83073 bacillus ce  
O9KMS3 klebsiella  
C475C5 escherichia  
O8G112 borellia bu  
O8G104 borellia bu  
O8Mfy6 taraxacum (   
P93233 lycopersico  
O63668 rattus norv  
O67113 influenzavi  
O07624 rous sarcom  
O08433 rattus sp.  
O8G100 borellia bu  
O8nhh7 homo sapien  
Q15897 homo sapien  
P92214 arablyopyrum  
P92393 hordeum vul  
P924C3 isophopyrum  
P92427 peridictyon  
O99182 gnatholebia  
P92430 aegilops ta  
P92221 bromus iner  
P92425 pseudorcegr  
P92381 hordeum bra

ALIGNMENTS

RESULT 1  
P70804  
ID P70804 PRELIMINARY; PRT; 7 AA.  
AC P70804;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ALGT protein (Fragment).  
GN ALGT.  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A., Ertesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in Pseudomonas aeruginosa.";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AEDC CRC64;

Query Match 50.0%; Score 16; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred.No. 8.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7  
|:|:  
2 TVSS 5

RESULT 2

O34028

ID O34028 PRELIMINARY; PRT; 7 AA.

AC O34028;

DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Catechol-2,3-dioxygenase (Fragment).  
 GN PRNE.  
 OS Sphingomonas chunghuensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
 OC Sphingomonadaceae; Sphingomonas.  
 OX NCBI\_TaxID=56193;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DJ77;  
 RA Kim Y.-C.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U88298; AAB66311.1; -.  
 KW Dioxxygenase.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 968 MW; 72A452D1A699D46C CRC64;

Query Match 37.5%; Score 12; DB 2; Length 7;  
 Best Local Similarity 20.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 4; Mismatches 3; Indels 3; Gaps 0;

QY 3 LTI 3  
 Db 3 FDL 7

RESULT 3  
 Q54248 PRELIMINARY; PRT; 7 AA.  
 ID Q54248  
 AC Q54248;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RplC protein (Fragment).  
 GN RPLC.  
 OS Streptomyces griseus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptoryciaceae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1321;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N2-3-11;  
 RX MEDLINE=20011291; PubMed=10542330;  
 RA Poehling S., Piepersberg W., Wehmeier U.P.;  
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus  
 N2-3-11 and interaction of the SecY protein with the SecA protein.";  
 RL Biochim. Biophys. Acta 1447:298-302(1999).  
 DR EMBL; X95915; CAA65160.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2AC CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTI 4  
 Db 2 TVT 4

RESULT 4  
 O07354 PRELIMINARY; PRT; 7 AA.  
 ID O07354  
 AC O07354;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NifK (Fragment).  
 GN NIFK.  
 OS Synethococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).  
 CC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.

OX NCBI\_TaxID=41432;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RF-1;  
 RX MEDLINE=99231861; PubMed=10217509;  
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;  
 RT "Organization and expression of nitrogen-fixation genes in the aerobic  
 nitrogen-fixing unicellular cyanobacterium Synethococcus sp. strain  
 RF-1.";  
 RL Microbiology 145:743-753(1999).  
 DR EMBL; AF003700; AAC35193.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B03C CRC64;

Query Match 28.1%; Score 9; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 Db 3 FDL 5

RESULT 5  
 F82445 PRELIMINARY; PRT; 7 AA.  
 ID F82445  
 AC F82445;  
 DT 01-JUN-2000 (TREMBLrel. 14, Created)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 10 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 CC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture.";  
 RL Planta 200-0(2000).  
 CC -:- SUBCELLULAR LOCATION: CELL WALL.  
 CC -:- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2AC CRC64;

Query Match 28.1%; Score 9; DB 10; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTI 5  
 Db 1 VTV 3

RESULT 6  
 Q8JE81 PRELIMINARY; PRT; 7 AA.  
 ID Q8JE81  
 AC Q8JE81;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN POL.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=4874;  
 RX MEDLINE=22056123; PubMed=12060770;  
 RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
 RA Hoffmann D., Korn K., Selbig C.;  
 RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics  
 RT approach to predicting phenotype from genotype.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).  
 DR EXBL: AF347267; AAK32344.1; ..  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 555 MW; 76C37731A046C700 CRC64;

Query Match 29.1%; Score 9; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
 Db 4 TL 5

## RESULT 7

P8218:  
 ID P82181 PRELIMINARY; PRT; 6 AA.  
 AC P82181;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=cv. ALVARO; TISSUE=Leaf;  
 RX MEDLINE=20435798; PubMed=10874046;

RA Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the 50 S subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 275:28466-28482(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR001790; Ribosomal\_L10.  
 DR InterPro: IPR002363; Ribosomal\_L10eub.  
 DR Pfam: PFC0466; Ribosomal\_L10; PARTIAL.  
 DR PROSITE: PS01109; RIBOSOMAL\_L10; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 8; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IS 6  
 Db 2 IS 3

## RESULT 8

P82182:  
 ID P82182 PRELIMINARY; PRT; 6 AA.  
 AC P82182;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;  
 RX MEDLINE=20435798; PubMed=10874046;  
 RA Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the 50 S subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 275:28466-28482(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR001790; Ribosomal\_L10.  
 DR InterPro: IPR002363; Ribosomal\_L10eub.  
 DR Pfam: PFC0466; Ribosomal\_L10; PARTIAL.  
 DR PROSITE: PS01109; RIBOSOMAL\_L10; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 8; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IS 6  
 Db 2 IS 3

## RESULT 9

P72081:  
 ID P72081 PRELIMINARY; PRT; 7 AA.  
 AC P72081;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 3'-methylcephem hydroxylase (Fragment).  
 GN CEFF.  
 OS Nocardia lactamdurans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=1913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96009872; PubMed=7557411;  
 RA Coque J., Perez-Llarena F.J., Enguita F.J., Puente J.L., Martin J.F.,  
 RA Liras P.;  
 RT "Characterization of the cmh genes of Nocardia lactamdurans and  
 RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem  
 RL O-carbamoyltransferase for cephamycin biosynthesis.";  
 RL Gene 162:21-27(1995).  
 DR EXBL: Z21682; CAA79797.1; ..  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 25.0%; Score 9; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7  
 Db 5 VTS 7

## RESULT 10

Q47029:  
 ID Q47029 PRELIMINARY; PRT; 7 AA.  
 AC Q47029;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Aad A1 protein (Fragment).  
 GN Aad A1.  
 OS Enterobacter cloacae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 ON NCBI\_TaxID=550;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94079349; PubMed=8257126;  
 RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;  
 RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-acetyltransferase";  
 RT acetyltransferase";  
 RL Antimicrob. Agents Chemother. 37:2074-2079(1993).  
 RL EMBL; M88012; AAA:6193.1; --  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 21.9%; Score 7; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LT 4  
 :  
 1 IT 2

RESULT 11  
 Q65578 PRELIMINARY; PRT; 7 AA.  
 ID Q65578  
 AC Q65578;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 6.8 kDa protein (fragment).  
 OS Bovine herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 ON NCBI\_TaxID=10120;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Cooper;  
 RX MEDLINE=95313343; PubMed=7793062;  
 RA Vitek C., Banes V., Lu Z., Kutish G.F., Paces V., Rock D.,  
 RA Letcworth G., Schwyer M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus.";  
 RL Virology 210:100-108(1995).  
 RL EMBL; Z48053; CAA88130.1; --  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 758 MW; 6D33455B1F1B1CC CRC64;

Query Match 21.9%; Score 7; DB 12; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TISS 7  
 :  
 1 TTHS 4

RESULT 12  
 P83308 PRELIMINARY; PRT; 5 AA.  
 ID P83308;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE FMRamide-like neuroptide (LPLAF-amide).  
 OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 ON NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX PubMed=6137771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRPamide.";  
 RL Nature 305:328-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRP-AMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400C00 CRC64;

Query Match 18.8%; Score 6; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 :  
 5 F 5

RESULT 13  
 P82541 PRELIMINARY; PRT; 6 AA.  
 ID P82541  
 AC P82541;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S19 beta (fragment).  
 OS Spinacia oleracea (Spinach).  
 CC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 ON NCBI\_TaxID=3562;  
 RN (1)  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC STRAIN=cv. ALVARO; TISSUE=leaf;  
 RX MEDLINE=20435797; PubMed=10674039;  
 RA Yamaguchi K., von Kroblach K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the small subunit of an organelle ribosome (chloroplast)";  
 RL J. Biol. Chem. 37:28455-28465(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.  
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.  
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA  
 CC FORM IS THE MINOR BASIC FORM.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR002222; Ribosomal S19.  
 DR Pfam; PF00203; Ribosomal S19; PARTIAL.  
 DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.  
 DR PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON TER 6  
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 18.8%; Score 6; DB 10; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TIS 6  
 :  
 1 TRS 3



Search completed: October 4, 2003, 12:48:31  
Job time : 50 secs

RESULT 14

OS0556 PRELIMINARY: PRT: 7 AA.  
AC OS0556;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE GLYA (Fragment).  
GN GLYA.  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
OS actinomycetemcomitans).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33384;  
RX MEDLINE=96355846; PubMed=8751884;  
RA Kolodrubetz E., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
RA Kraig E.;  
RT "cis Elements and trans factors are both important in strain-specific  
RT regulation of the leukotoxin gene in Actinobacillus  
RT actinomycetemcomitans.";  
RL Infect. Immun. 64:3451-3460(1996).  
DR EMBL; U51862; AAB88721.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D76734C420 CRC64;

Query Match 18.8%; Score 6; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTI 5  
|  
Db 3 LPV 5

RESULT 15

OS0556 PRELIMINARY: PRT: 7 AA.  
AC OS0556;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN TN-A.  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=143777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CH2-4;  
RX MEDLINE=21604134; PubMed=11763242;  
RA Mindlin S.Z., Kolodii G.Y., Gorienko Z.M., Mirakhina S.V.,  
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,  
RA Yurieva O.V., Nikiforov V.G.;  
RT "Mercury resistance transposons of Gram-negative environmental  
RT bacteria and their classification.";  
RL Res. Microbiol. 152:811-822(2001).  
DR EMBL; AJ302778; CAC83058.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1C46DAA9A0 CRC64;

Query Match 18.8%; Score 6; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:26:27 / Search time 51.6667 seconds  
(without alignments)  
21,505 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTLTSS ?

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107563 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 75613

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:	5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:	6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:	8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:	9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:
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22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:	23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:	24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length DB	ID	Description
1	28	87.5	7	20	AAV40738 S4 derivative #12, Scaffold protein S
2	28	87.5	7	21	AAB30076 S4 derivative #11, Scaffold protein S
3	25	78.1	7	20	AAV40737 S4 derivative #10, Scaffold protein S
4	25	78.1	7	21	AAB30075 S4 derivative #9, Scaffold protein S
5	24	75.0	7	20	AAV40736 S4 derivative #8, Scaffold protein S
6	24	75.0	7	21	AAB30074 S4 derivative #7, Scaffold protein S
7	21	65.6	7	20	AAV40735 Human colon specific
8	21	65.6	7	21	AAB30073
9	20	62.5	5	23	AAU85454

10	19	59.4	6	22	AAV51422 Integrin activatin
11	18	56.2	7	19	AAW58711 tryptic 40 kD subu
12	18	56.2	7	21	AAV64225 Cacharin-related n
13	18	56.2	7	23	ABB84102 Human single chain
14	17	53.1	5	24	ABJ12234 Streptococcal prot
15	17	53.1	5	24	ABJ12235 Streptococcal prot
16	17	53.1	6	18	AAW39453 Human T cell epito
17	17	53.1	6	19	AAW75358 Hexapeptide #13 bi
18	17	53.1	6	19	AAW75290 Hexapeptide #13 bi
19	17	53.1	6	24	AAE31832 Androgen receptor
20	17	53.1	7	11	AAW37656 Ribonuclease reduc
21	17	53.1	7	20	AAV40723 S3 derivative #20
22	17	53.1	7	21	AAB30062 Scaffold protein S
23	17	53.1	7	22	AAW44200 H11 binding site c
24	17	53.1	7	22	AAW44205 H11 binding site c
25	16	50.0	6	10	AAW93345 Portion of myc var
26	16	50.0	6	17	AAW93089 GAL4 DNA binding d
27	16	50.0	6	19	AAW76753 Murine signalling
28	16	50.0	6	19	AAW61443 Gal 4 protein, 3'
29	16	50.0	6	20	AAW92487 Murine Gal4 prote
30	16	50.0	6	21	AAB03571 Nuclear chimera co
31	16	50.0	6	21	AAV90491 GAL4 DNA binding d
32	16	50.0	6	22	AAB60836 Peptide #16 encode
33	16	50.0	6	22	AAB36961 Peptide #2 encode
34	16	50.0	6	23	AAE28111 Human immunoglobul
35	16	50.0	6	23	ABJ11455 Kur-an 125P5C8 epit
36	16	50.0	6	24	ABR44966 Staphylococcus aur
37	16	50.0	6	24	ABR45358 Staphylococcus aur
38	16	50.0	6	24	ABR45694 Staphylococcus aur
39	16	50.0	6	24	ABR46086 Staphylococcus aur
40	16	50.0	6	24	ABR46478 Staphylococcus aur
41	16	50.0	6	24	ABR4687C Staphylococcus aur
42	16	50.0	7	16	AAW72775 Mamalian ribonucle
43	16	50.0	7	20	ABB76923 Cyclodextrin glucos
44	16	50.0	7	20	AAV42013 Rheumatoid arthrit
45	16	50.0	7	20	AAV40625 S1 derivative #6,

ALIGNMENTS

RESULT 1  
AAV40738  
ID AAV40738 standard; peptide; 7 AA.  
XX  
AC AAV40738;  
XX 01-DEC-1999 (first entry)  
XX S4 derivative #12, beta strand of scaffold protein structure.  
DE Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
XX tumour; chemotherapeutic agent.  
KW Synthetic.  
CS  
XX  
PN EP947582-A1.  
XX  
PD 06-OCT-1993.  
XX  
PF 31-MAR-1998; 98EP-0870065.  
XX  
PR 31-MAR-1998; 98EP-0870065.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
FI Desmet J, Hufton S, Hoogenboom H, Sablon E;  
XX  
DR WPI; 1999-542958/46.  
XX  
PT New scaffold protein, useful for stabilizing antigens used as vaccines  
XX

```
PS Disclosure; Page 6; 105pp; English.
XX
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.
XX
SQ Sequence 7 AA;
Query Match 87.5%; Score 28; DB 20; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db 2 FTLTIS 7

RESULT 2
AAB30076
ID AAB30076 standard; Peptide; 7 AA.
XX
AC AAB30076;
XX
DT 09-FEB-2001 (first entry);
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 137.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060370-A1.
XX
PJ 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP02283.
XX
PR 01-APR-1999; 99WO-EP02283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
WPI; 2000-665002/64.
XX
Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments
XX
```

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PS Disclosure; Page 15; 68pp; English.
XX
CC The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB32930-B29939 were used in the
CC production of the proteins of the invention.
XX
SQ Sequence 7 AA;
Query Match 87.5%; Score 28; DB 21; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db 2 FTLTIS 7

RESULT 3
AAY40737
ID AAY40737 standard; peptide; 7 AA.
XX
AC AAY40737;
XX
DT 01-DEC-1999 (first entry);
XX
DE S4 derivative #11, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PJ 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-0870065.
XX
PR 31-MAR-1998; 98EP-0870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
WPI; 1999-542958/46.
XX
New scaffold protein, useful for stabilizing antigens used as vaccines
PT
XX
Disclosure; Page 6; 105pp; English.
XX
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
```

target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines.

Sequence 7 AA;

Query Match 78.1%; Score 25; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 FTLTIS 6  
:|||||  
2 YTLTIS 7

RESULT 4  
AAB30075  
D AAB30075 standard; Peptide; 7 AA.  
C AAB30075;  
X  
X C9-FEB-2001 (first entry)  
T Scaffold protein SCA S4 peptide SEQ ID NO: 136.  
X  
X Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
X SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
X diabetic retinopathy; atherosclerosis.  
X Synthetic.  
X WO2000060070-A1.  
X 12-OCT-2000.  
X 01-APR-1999; 99WO-EP02283.  
X 01-APR-1999; 99WO-EP02283.  
X (INNO-) INNOGENETICS NV.  
X Desmet J, Hufton S, Hoogenboom H, Sablon E;  
X WPI; 2000-665002/64.  
X Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments -  
X Disclosure; Page 15; 68pp; English.  
X The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention.

Sequence 7 AA;

Query Match 78.1%; Score 25; DB 21; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 FTLTIS 6  
:|||||  
2 YTLTIS 7

RESULT 5  
AAY40736  
ID AAY40736 standard; peptide; 7 AA.  
XX  
AC AAY40736;  
XX  
DT 01-DEC-1999 (first entry)  
XX  
DE S4 derivative #10, beta strand of scaffold protein structure.  
XX  
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.  
XX  
OS Synthetic.  
XX EP947582-A1.  
XX PD 06-OCT-1999.  
XX 31-MAR-1998; 98EP-0870065.  
XX 31-MAR-1998; 98EP-0870065.  
XX (INNO-) INNOGENETICS NV.  
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;  
XX WPI; 1999-542958/46.  
XX New scaffold protein, useful for stabilizing antigens used as vaccines  
PT -  
XX Disclosure; Page 6; 105pp; English.

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines.

Sequence 7 AA;

Query Match 75.0%; Score 24; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6  
:|||||  
DB 2 FTLTIS 7

RESULT 6  
AAB30074

ID XX AAB30074 standard; Peptide; 7 AA.  
AC AAB30074;  
XX  
DT 09-FEB-2001 (first entry)  
XX  
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.  
XX  
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
KW diabetic retinopathy; atherosclerosis.  
XX  
OS Synthetic.  
XX  
PN WO200060070-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 01-APR-1999; 99WO-EP02283.  
XX  
PR 01-APR-1999; 99WO-EP02283.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;  
XX  
DR WPI; 2000-665002/64.  
XX  
PT Scaffold composed of single-chain polypeptide having beta sandwich  
PT architecture carrying new and randomized peptide sequences useful as  
PT supporting framework and carrying antigen- or receptor binding  
PT fragments -  
XX  
XX Disclosure; Page 15; 68pp; English.  
PS  
XX The present invention is concerned with producing scaffold proteins  
XX based upon the human CTLA-4 SCA domain. These scaffold proteins can be  
XX used as a scaffold to bind antigen- or receptor-binding fragments. These  
XX can be used in the treatment of diseases such as cancer,  
XX atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and  
XX diabetic retinopathy. Sequences AAB29930-B29939 were used in the  
XX production of the proteins of the invention.  
SQ  
Sequence 7 AA;  
Query Match 75.0%; Score 24; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLLIS 6  
Db 1 :|||  
2 FTLSIS 7

RESULT 7  
AAY40735  
ID AAY40735 standard; peptide; 7 AA.  
XX  
AC AAY40735;  
XX  
DT 01-DEC-1999 (first entry)  
XX  
DE S4 derivative #9, beta strand of scaffold protein structure.  
XX  
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
KW tumour; chemotherapeutic agent.  
XX  
OS Synthetic.  
XX  
PN EP947582-A1.  
XX  
PD 06-OCT-1999.  
XX

PF 31-MAR-1998; 98EP-C870365.  
XX  
PR 31-MAR-1998; 98EP-C870365.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;  
XX  
DR WPI; 1999-542958/46.  
XX  
PT New scaffold protein, useful for stabilizing antigens used as vaccines  
PT  
XX  
PS Disclosure; Page 6; 105pp; English.  
XX  
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the  
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a  
CC beta strand peptide which forms part of a beta sheet. Peptides  
CC (AAY40601-Y40609) together form a single-chain scaffold protein which  
CC contains at least 1 disulfide bond, contains less than 10% alpha helix  
CC and contains at least 6 beta-strands. The scaffold protein is constructed  
CC of beta strands Si-S6, and may also include beta strands A1-A3, or any  
CC functionally equivalent derivative of these sequences. The beta strands  
CC form two beta sheets Si/S4/S3 and S6/S5/S2 with each strand connected to  
CC the next by hydrogen bonds, which generate a beta sandwich architecture.  
CC If the additional beta strands A1-A3 are included in the structure the  
CC scaffold is constructed of two beta sheets, with the structures  
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each  
CC other via amino acid loops, where at least one of the loops binds to a  
CC receptor or antigen. The scaffold protein is used to stabilize antigens  
CC or whole proteins such as receptors, or their fragments. It may be used  
CC to bind two separate molecules. For example, one surface of the scaffold  
CC may be bound to a protein which binds to a tumour antigen. This will  
CC target the complex to tumour cells. Another surface may be bound to a  
CC cytotoxic molecule or an autoimmune antibody which may then kill the  
CC tumour cells. Therefore the scaffold protein may be used to target  
CC chemotherapeutic agents to specific cells. It may also be used to  
CC stabilize individual peptides in a peptide library and may be used in  
CC diagnostic techniques, and to stabilize antigens used as vaccines.  
XX  
SQ Sequence 7 AA;  
Query Match 65.6%; Score 21; DB 20; Length 7;  
Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLLIS 6  
Db 1 :|||  
2 YSLTIS 7

RESULT 8  
AAB30073  
ID AAB30073 standard; Peptide; 7 AA.  
XX  
AC AAB30073;  
XX  
DT 09-FEB-2001 (first entry)  
XX  
DE Scaffold protein SCA S4 peptide SEQ ID NO: 134.  
XX  
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
KW diabetic retinopathy; atherosclerosis.  
XX  
OS Synthetic.  
XX  
PN WO200060070-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 01-APR-1999; 99WO-EP02283.  
XX

PR 01-APR-1999; 99WO-EP02283.  
XX (INNO-) INNOGENETICS NV.  
XX Desmet J, Hufton S, Hoogenboom H, Sabien B;  
XX WPI; 2000-665002/64.  
XX Scaffold composed of single-chain polypeptide having beta sandwich  
XX architecture carrying new and randomized peptide sequences useful as  
XX supporting framework and carrying antigen- or receptor binding  
XX fragments -  
XX Disclosure; Page 15; 48pp; English.  
XX The present invention is concerned with producing scaffold proteins  
XX based upon the human CUA-4 SCA domain. These scaffold proteins can be  
XX used as a scaffold to bind antigen- or receptor-binding fragments. These  
XX can be used in the treatment of diseases such as cancer,  
XX atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and  
XX diabetic retinopathy. Sequences AAB29930-B29939 were used in the  
XX production of the proteins of the invention.  
XX Sequence 7 AA;  
SQ

Query Match 65.6%; Score 21; DB 21; Length 7;  
Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLTIS 6  
Db 2 YSLTIS 7

RESULT 9  
AAU85454  
ID AAU85454 standard; Peptide; 5 AA.  
XX AC AAU85454;  
XX XX  
XX DT 21-MAY-2002 (first entry)  
XX DE Human colon specific polypeptide antibody binding site #31.  
XX KW Human; colon specific gene; CSG; cytostatic; metastasis;  
XX QW colon cancer staging; antibody binding site.  
XX OS Homo sapiens.  
XX OS  
XX PN WO200206515-A2.  
XX YX 24-JAN-2002.  
XX PD  
XX PF 17-JUL-2001; 2001WO-US22454.  
XX PR 17-JUL-2002; 2000US-0618596.  
XX XX  
XX PA (DIAD-) DIADEXUS INC.  
XX PI Macina RA, Sun Y;  
XX XX  
XX WPI; 2002-171815/22.  
XX DR  
XX XX  
XX PT Diagnosing, staging or monitoring colon cancer involves determining a  
XX PT colon specific gene in cells, tissues or body fluids in patient; and  
XX PT comparing it with levels of the gene from a normal human control -  
XX XX  
XX PS Disclosure; Page 21; 52pp; English.  
XX XX  
XX The invention relates to diagnosing the presence of colon cancer,  
XX CC metastases of colon cancer, staging colon cancer, monitoring colon cancer  
XX CC for the onset of metastasis or monitoring a change in stage of colon  
XX CC cancer in a patient. The method involves determining a colon specific

CC gene (CSG) in cells, tissues or bodily fluids and comparing it with  
CC levels of CSG in cells, tissues or bodily fluids from a normal human  
CC control. Colon cancer can be treated by administering a molecule which  
CC down regulates the expression or activity of CSG. An immune response  
CC against a target cell expressing CSG can be induced by delivering an  
CC immunologically stimulatory amount of a CSG protein to a patient, so that  
CC an immune response is mounted. Therapeutic agents are useful for imaging  
CC colon cancer in a patient by administering an agent labeled with  
CC paramagnetic ions or a radioisotope to the patient. They are also useful  
CC for preventing the onset of colon cancer, and in diagnosis and treatment  
CC of the disease. Sequences AAU85424-AAU85502 represent human colon  
CC specific protein antibody binding sites used in the method of the  
XX invention.  
XX Sequence 5 AA;  
SQ

Query Match 62.5%; Score 20; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLT 4  
Db 2 FTLT 5

RESULT 10  
AAU51422  
ID AAU51422 standard; peptide; 6 AA.  
XX AC AAU51422;  
XX XX  
XX DT 08-JAN-2002 (first entry)  
XX DE Integrin activating peptide SEQ ID NO 1.  
XX KW Integrin stimulant; vulnery; injury healing;  
XX KW postsurgical tissue recovery.  
XX OS Unidentified.  
XX XX  
XX PN JP2001213898-A.  
XX XX  
XX PD 07-AUG-2001.  
XX XX  
XX PF 31-JAN-2000; 2000JP-0022469.  
XX XX  
XX PR 31-JAN-2000; 2000JP-0022469.  
XX XX  
XX PA (HISM) HISAMITSU PHARM CO LTD.  
XX XX  
XX DR WPI; 2001-629610/73.  
XX XX  
XX PT An injury healing and postsurgical tissue recovering integrin  
XX PT activating peptide -  
XX PS Claim 1; Page 3; 11pp; Japanese.  
XX XX  
XX CC The invention relates to novel peptides with vulnery activity, useful  
XX CC for injury healing and postsurgical tissue recovery by acting as an  
XX CC integrin stimulant.  
XX XX  
XX SQ Sequence 6 AA;  
SQ

Query Match 59.4%; Score 19; DB 22; Length 6;  
Best Local Similarity 60.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLTI 5  
Db 1 YTLTI 5

RESULT 11







RESULT 15  
ABU12235  
ID ABU12235 standard; Peptide; 5 AA.  
XX  
AC ABU12235;  
XX  
DT 19-FEB-2003 (first entry)  
XX  
DE Streptococcal protein G, 1GB1, alpha helix prediction pentapeptide #52.  
KW  
KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;  
atomistic modelling; low energy conformation; entropic energy;  
free energy; equilibrium probability; helical cluster; integer-linear;  
mathematical model; hydrophobic contact energy;  
atom force field potential; global optimisation; torsion angle;  
dynamic algorithm; three-dimensional structure; tertiary structure;  
immunoglobulin-binding domain; protein G; 1GB1.  
XX  
OS Streptomyces griseus.  
XX  
PN WO200279872-A2.  
XX  
FD 10-OCT-2002.  
XX  
PF 19-FEB-2002; 2002WO-JSC4644.  
XX  
PR 16-FEB-2002; 2001US-0788006.  
XX  
PA (UYPR-) UNIV PRINCETON.  
XX  
Pz Floudas CA, Klepeis JL;  
XX  
DR WPI; 2003-058449/05.  
XX  
PT Determining helix regions, and beta sheets of polypeptide, involves  
partitioning peptide, atomistic modeling by selected force, generating  
ensemble low energy, and calculating free energies for each peptide -  
XX  
PS Example 1; Page 59; 147pp; English.  
XX  
CC The invention discloses a ASTRO-FOLD approach for the ab initio  
prediction method for determining the existence and location of  
alpha-helix regions and arrangement of beta-sheets and disulphide bridges  
of a polypeptide. The method comprises defining the first segment of the  
amino acid sequence, performing atomistic modelling upon each segment,  
generating an ensemble of low energy conformations, determining the  
entropic and free energy for each segment and then ascertaining the  
equilibrium probabilities for helical clusters. The segments consist of  
pentapeptides, with each further segment including a majority of the  
amino acid residues of the first segment, together with an additional  
amino acid residue(s), adjacent to the first amino acid sequence. The  
beta-sheets and disulphide bridges of a polypeptide are determined by  
identifying a superstructure encompassing alternative beta-strand  
arrangements, representing the superstructure by an integer-linear  
programming mathematical model, with the model maximising the total  
hydrophobic contact energy, and then solving the model. The method can  
also apply energy modelling with a full atom force field potential to  
generate a constrained global optimisation problem, optionally applying a  
torsion angle dynamics algorithm and then solving the constrained global  
optimisation problem to determine the three-dimensional structure of the  
polypeptide. The method is useful for determining the tertiary structure  
of a polypeptide and is accurate and reliable. The sequences presented in  
ABU12184-ABU12235 are the pentapeptides of the Streptomyces griseus  
immunoglobulin-binding domain from streptococcal protein G, 1GB1, which  
were used to predict the alpha-helical regions in an example of the  
method of the invention.

XX SQ Sequence 5 AA;

Query Match 53.1%; Score 17; DB 24; Length 5;  
Best Local Similarity 75.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVLT 4  
Db 1 FVLT 4

Search completed: October 4, 2003, 12:45:22  
Job time : 53.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:48:43 ; Search time 31.6667 Seconds  
(without alignments)  
32.896 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_5/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_5/ptodata/1/pubpaa/PCI\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US05\_PUBCOMB.pep.\*
- 5: /cgn2\_5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US0A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US0B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	56.2	7	15	US-10-006-869-637 Sequence 637, App
2	17	53.1	5	11	US-09-788-006-107 Sequence 107, App
3	17	53.1	5	11	US-09-788-006-108 Sequence 108, App
4	17	53.1	5	15	US-10-154-971-29 Sequence 29, Appl
5	17	53.1	6	10	US-09-777-921A-17 Sequence 17, Appl
6	17	53.1	6	11	US-09-530-139-14 Sequence 14, Appl
7	17	53.1	6	14	US-10-156-820-59 Sequence 59, App
8	17	53.1	5	15	US-10-097-175-97 Sequence 97, Appl
9	16	50.0	4	12	US-10-159-006-47 Sequence 47, Appl
10	16	50.0	7	9	US-09-832-723-69 Sequence 69, App
11	16	50.0	7	10	US-09-996-288-164 Sequence 164, App
12	16	50.0	7	11	US-09-996-265-164 Sequence 164, App
13	16	50.0	7	12	US-10-303-331-69 Sequence 69, Appl
14	16	50.0	7	12	US-10-022-066-214 Sequence 214, App
15	15	46.9	5	12	US-10-286-186-3 Sequence 3, Appl

16	15	46.9	5	12	US-10-286-186-4	Sequence 4, Appl
17	15	46.9	5	12	US-10-315-964A-394	Sequence 394, App
18	15	46.9	5	12	US-10-317-251A-394	Sequence 394, App
19	15	46.9	5	12	US-10-317-252A-394	Sequence 394, App
20	15	46.9	6	9	US-09-876-388-6	Sequence 6, Appl
21	15	46.9	6	12	US-10-315-964A-402	Sequence 402, App
22	15	46.9	6	12	US-10-317-251A-402	Sequence 402, App
23	15	46.9	6	12	US-10-317-252A-402	Sequence 402, App
24	15	46.9	6	15	US-10-105-930-39	Sequence 39, Appl
25	15	46.9	6	15	US-10-006-869-650	Sequence 650, App
26	15	46.9	6	15	US-10-287-892-6	Sequence 6, Appl
27	15	46.9	6	15	US-10-288-343-6	Sequence 6, Appl
28	15	46.9	7	9	US-09-056-163B-5	Sequence 5, Appl
29	15	46.9	7	9	US-09-056-163B-124	Sequence 124, App
30	15	46.9	7	9	US-09-876-388-7	Sequence 7, Appl
31	15	46.9	7	9	US-09-734-417-12	Sequence 12, Appl
32	15	46.9	7	10	US-09-095-881-8	Sequence 8, Appl
33	15	46.9	7	10	US-09-947-137-7	Sequence 7, Appl
34	15	46.9	7	10	US-09-996-288-133	Sequence 133, App
35	15	46.9	7	10	US-09-996-288-135	Sequence 135, App
36	15	46.9	7	10	US-09-996-288-160	Sequence 160, App
37	15	46.9	7	11	US-09-229-751A-53	Sequence 53, Appl
38	15	46.9	7	11	US-09-229-751A-54	Sequence 54, Appl
39	15	46.9	7	11	US-09-996-265-133	Sequence 133, App
40	15	46.9	7	11	US-09-996-265-135	Sequence 135, App
41	15	46.9	7	11	US-09-996-265-160	Sequence 160, App
42	15	46.9	7	12	US-10-169-351-81	Sequence 81, Appl
43	15	46.9	7	12	US-10-286-457-210	Sequence 210, App
44	15	46.9	7	14	US-10-050-552A-4	Sequence 4, Appl
45	15	46.9	7	15	US-10-006-869-651	Sequence 651, App

ALIGNMENTS

RESULT 1  
US-10-006-869-637  
; Sequence 637, Application US/1000869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 637  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative linear modulating agent based on  
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-006-869-637

Query Match 56.2%; Score 18; DB 15; Length 7;  
Best Local Similarity 57.1%; Pred. No. 5.3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY : FTLTISS 7

Db : FTLTISS 7

RESULT 2

US-09-788-006-107

; Sequence 107, Application US/09788006

; Publication No. US20030036093A1

```

; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107

Query Match          53.1%; Score 17; DB 11; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
Db 2 FTVT 5

RESULT 3
US-09-788-006-108
; Sequence 108, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-108

Query Match          53.1%; Score 17; DB 11; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
Db 1 FTVT 4

RESULT 4
US-10-154-971-29
; Sequence 29, Application US/10:154971
; Publication No. US2003008074A1
; GENERAL INFORMATION:
; APPLICANT: Hamers, Raymond
; Myldermans, Serge
; TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
; USE FOR THERAPEUTIC OR VETERINARY PURPOSES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENCER & FRANK
; STREET: 1100 New York Avenue, N.W., Suite 300 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3c
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,971
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP96/01725
; FILING DATE: 25-APR-1996
; APPLICATION NUMBER: EP 95400932.0
; FILING DATE: 25-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gollin, Michael A.
; REGISTRATION NUMBER: 31,957
; REFERENCE/DOCKET NUMBER: GUPLA 0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-414-4000
; TELEFAX: 202-414-4040
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-154-971-29

Query Match          53.1%; Score 17; DB 15; Length 5;
Best Local Similarity 60.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 1 VTVSS 5

RESULT 5
US-09-777-921A-17
; Sequence 17, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO01103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-17

Query Match          53.1%; Score 17; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 6
Db 2 LTISS 5

RESULT 6
US-09-530-139-14
; Sequence 14, Application US/09530139
; Publication No. US20030092892A1

```

; GENERAL INFORMATION:  
; APPLICANT: FRENKEN, LEON GERARDUS  
; APPLICANT: HOWELL, STEVEN  
; APPLICANT: LEDEBOER, ADRIANUS MARINUS  
; APPLICANT: VAN DER LOGT, CORNELIS PAUL  
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS  
; FILE REFERENCE: 60113/268075/ASH  
; CURRENT APPLICATION NUMBER: US/09/530,139  
; CURRENT FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: PCT/EP98/06991  
; PRIOR FILING DATE: 1998-12-27  
; PRIOR APPLICATION NUMBER: EP 97308529.4  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
JS-09-530-139-14

Query Match 53.1%; Score 17; DB 14; Length 6;  
Best Local Similarity 50.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 LTSS 7  
Db 2 TVSS 6

RESULT 7  
JS-10-156-820-59  
Sequence 59, Application US/10156820  
Publication No. US20020150358A1  
GENERAL INFORMATION:  
APPLICANT: Boulanger, Pierre  
APPLICANT: Hong, Saw See  
APPLICANT: Karayan, Lucie  
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
FILE REFERENCE: 032751-036  
CURRENT APPLICATION NUMBER: US/10/156,820  
CURRENT FILING DATE: 2002-06-30  
PRIOR APPLICATION NUMBER: PCT/FR98/00184  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: FR 97/01035  
PRIOR FILING DATE: 1997-01-30  
PRIOR APPLICATION NUMBER: FR 97/11166  
PRIOR FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 59  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Phagotome  
JS-10-156-820-59

Query Match 53.1%; Score 17; DB 14; Length 6;  
Best Local Similarity 75.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTLT 4  
b 3 YTLT 6

ESULT 8  
S-10-097-175-97  
Sequence 97, Application US/10097175

Publication No. US20030045680A1  
GENERAL INFORMATION:  
APPLICANT: JOYAL, JOHN L.  
APPLICANT: MUELLER, JOHN  
APPLICANT: OZA, VIBHA B.  
APPLICANT: FINDEIS, MARK A.  
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR  
FILE REFERENCE: PPI-110  
CURRENT APPLICATION NUMBER: US/10/097,175  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/275,240  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: 60/352,399  
PRIOR FILING DATE: 2002-01-29  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Androgen Receptor Binding Polypeptides  
US-10-097-175-97

Query Match 53.1%; Score 17; DB 15; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 LTSS 7  
Db 1 LTSS 5

RESULT 9  
US-10-159-006-47  
Sequence 47, Application US/10159006  
Publication No. US20030143229A1  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890002  
CURRENT APPLICATION NUMBER: US/10/159,006  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 09/301,593  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: EP 98107925.4  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: US 60/086,049  
PRIOR FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 47  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-159-006-47

Query Match 50.0%; Score 16; DB 12; Length 4;  
Best Local Similarity 75.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LTSS 7  
Db 1 TVSS 4

RESULT 10  
JS-09-832-723-69

; Sequence 69, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; APPLICANT: Chen, Yiyou  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-09-832-723-69

Query Match 50.0%; Score 16; DB 9; Length 7;  
Best Local Similarity 75.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTI 5  
|:|  
Db 2 TITI 5

RESULT 11  
US-09-996-288-164  
; Sequence 164, Application US/99996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 164  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-164

Query Match 50.0%; Score 16; DB 10; Length 7;  
Best Local Similarity 50.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLTISS 7  
|:|  
Db 2 TMKLSS 7

RESULT 12  
US-09-996-265-164  
; Sequence 164, Application US/99996265  
; Publication No. US2003009584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 164  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-164

Query Match 50.0%; Score 16; DB 11; Length 7;  
Best Local Similarity 50.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLTISS 7  
|:|  
Db 2 TMKLSS 7

RESULT 13  
US-10-303-331-69  
; Sequence 69, Application US/10303331  
; Publication No. US20030152976A1  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Winetzky, Deborah S.  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-3  
; CURRENT APPLICATION NUMBER: US/10/303,331  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: US 09/832,723  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-10-303-331-69

Query Match 50.0%; Score 16; DB 12; Length 7;  
Best Local Similarity 75.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTI 5  
|:|  
Db 2 TITI 5

RESULT 14  
US-10-022-066-214  
; Sequence 214, Application US/10022066  
; Publication No. US20030166057A1  
; GENERAL INFORMATION:  
; APPLICANT: HILDEBRAND, WILLIAM H.  
; APPLICANT: PRILLMAN, KILEY RAE  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 6680.034  
; CURRENT APPLICATION NUMBER: US/10/022,066  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 09/465,321

PRIOR FILING DATE: 1999-12-17  
PRIOR APPLICATION NUMBER: 09/974,366  
PRIOR FILING DATE: 2001-10-10  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 214  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-10-022-066-214

Query Match: 50.0%; Score 16; DB 12; Length 7;  
Best Local Similarity 50.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TMTAAS 7  
Db 1 TMTAAS 6

RESULT 15  
JS-10-286-186-3  
Sequence 3, Application JS/10286186  
Publication No. JS20030143741A1  
GENERAL INFORMATION:  
APPLICANT: PALMER, KENNETH E.  
APPLICANT: FOGUE, GARY P.  
TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION  
TITLE OF INVENTION: VECTOR  
FILE REFERENCE: 00801017900US00  
CURRENT APPLICATION NUMBER: US/10/286,186  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: JS/09/505,477  
PRIOR FILING DATE: 2000-02-16  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Circovirus  
US-10-286-186-3

Query Match: 46.9%; Score 15; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTL 3  
Db 1 FTL 3

Search completed: October 4, 2003, 13:05:03  
Job time : 34.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:42:47 ; Search time 17 Seconds  
(without alignments)  
17.422 Million cell updates/sec

Title: US-09-712-819C-1  
Perfect score: 32  
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 49738

Minimum DB seq length: 3  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	18	56.2	7	4	US-09-187-859-637
2	18	56.2	7	4	US-09-839-542B-637
3	17	53.1	5	3	US-08-757-177-16
4	17	53.1	6	4	US-09-155-613A-59
5	17	53.1	6	4	US-09-266-805-5
6	17	53.1	7	2	US-08-739-401A-6
7	16	50.0	4	3	US-08-860-904-9
8	16	50.0	4	4	US-09-301-593-47
9	16	50.0	6	1	US-08-252-995D-7
10	16	50.0	6	2	US-08-478-386A-46
11	16	50.0	6	2	US-08-292-597-46
12	16	50.0	6	2	US-08-388-653-46
13	16	50.0	6	2	US-08-473-985-46
14	16	50.0	6	2	US-08-834-108-7
15	16	50.0	6	2	US-08-483-898-46
16	16	50.0	6	3	US-09-087-716-46
17	16	50.0	6	3	US-09-157-753-46
18	16	50.0	6	3	US-09-157-230-46
19	16	50.0	6	3	US-09-087-811-46
20	16	50.0	6	3	US-09-156-855-46
21	16	50.0	6	3	US-09-158-010-46
22	16	50.0	6	3	US-09-087-647-46
23	16	50.0	6	4	US-09-302-529-46
24	16	50.0	7	1	US-08-136-743B-55
25	16	50.0	7	2	US-08-177-109A-7
26	16	50.0	7	2	US-08-667-706-7
27	16	50.0	7	3	US-09-040-216-28

28	15	46.9	5	1	US-08-136-743B-63	Sequence 63, Appl
29	15	46.9	5	2	US-08-667-001-22	Sequence 22, Appl
30	15	46.9	5	3	US-09-040-216-55	Sequence 55, Appl
31	15	46.9	5	3	US-08-591-632-17	Sequence 17, Appl
32	15	46.9	5	3	US-08-591-632-23	Sequence 23, Appl
33	15	46.9	5	3	US-08-591-632-26	Sequence 26, Appl
34	15	46.9	5	4	US-09-611-451-17	Sequence 17, Appl
35	15	46.9	5	4	US-09-611-451-23	Sequence 23, Appl
36	15	46.9	5	4	US-09-611-451-26	Sequence 26, Appl
37	15	46.9	6	1	US-08-136-743B-62	Sequence 62, Appl
38	15	46.9	6	1	US-08-297-731-4	Sequence 4, Appl
39	15	46.9	6	1	US-08-290-448A-41	Sequence 41, Appl
40	15	46.9	6	1	US-08-290-448A-41	Sequence 41, Appl
41	15	46.9	6	1	US-08-175-369A-41	Sequence 41, Appl
42	15	46.9	6	2	US-08-622-720A-8	Sequence 8, Appl
43	15	46.9	6	3	US-09-040-216-54	Sequence 54, Appl
44	15	46.9	6	3	US-08-297-395-3	Sequence 3, Appl
45	15	46.9	6	3	US-09-146-675-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-187-859-637  
; Sequence 637, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C;  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 637  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative linear modulating agent based on  
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-09-187-859-637

Query Match 56.2%; Score 19; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLTISS 7  
||: ||  
Db 1 FTIDSSS 7

RESULT 2  
US-09-839-542B-637  
; Sequence 637, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 637  
; LENGTH: 7

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative linear modulating agent based on  
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion  
OTHER INFORMATION: recognition sequence  
US-09-839-5425-637

Query Match: 56.2%; Score 18; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLSSS 7  
Db 1 FTIDSS 7

RESULT 3  
US-08-757-177-16  
Sequence 16, Application US/08757177  
Patent No. 6071718  
GENERAL INFORMATION:  
APPLICANT: MUKERJI, PRADIP  
APPLICANT: HARDS, ROBERT G.  
APPLICANT: THURMOND, JENNIFER M.  
APPLICANT: LEONARD, AVANDA FUN-YEONG  
TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: One Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,177  
FILING DATE: 27-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,442  
REFERENCE/DOCKET NUMBER: 6004.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-935-1723  
TELEFAX: 847-938-2623  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-757-177-16

Query Match: 53.1%; Score 17; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7  
Db 2 TISS 5

RESULT 4  
US-09-155-613A-59  
Sequence 59, Application US/09155613A  
Patent No. 6420120

GENERAL INFORMATION:  
APPLICANT: Boulanger, Pierre  
APPLICANT: Hong, Saw See  
APPLICANT: Karavan, Lucie  
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
FILE REFERENCE: 032751-036  
CURRENT APPLICATION NUMBER: US/09/155,613A  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: PCT/FR96/30184  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: FR 97/01005  
PRIOR FILING DATE: 1997-01-30  
PRIOR APPLICATION NUMBER: FR 97/11166  
PRIOR FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 59  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Phagotome  
US-09-155-613A-59

Query Match: 53.1%; Score 17; DB 4; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4  
Db 3 YTLT 6

RESULT 5  
US-09-266-805-5  
Sequence 5, Application US/09266805  
Patent No. 6517829  
GENERAL INFORMATION:  
APPLICANT: Unilever N.V.  
APPLICANT: Unilever PLC  
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds  
TITLE OF INVENTION: provided with active antibodies  
FILE REFERENCE: t-7055  
CURRENT APPLICATION NUMBER: US/09/266,805  
CURRENT FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 5  
LENGTH: 6  
TYPE: PRT  
ORGANISM: llama  
US-09-266-805-5

Query Match: 53.1%; Score 17; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTVSS 7  
Db 2 VTVSS 6

RESULT 6  
US-08-739-401A-6  
Sequence 6, Application US/08739401A  
Patent No. 5837461  
GENERAL INFORMATION:  
APPLICANT: Neitz, Maureen E.  
APPLICANT: Neitz, John F.  
TITLE OF INVENTION: DETECTION OF CONE-PHOTORECEPTOR-BASED  
TITLE OF INVENTION: VISION DISORDERS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:



ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/05/739,4C1A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Baker, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 650053, 91151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5709  
TELEFAX: (414) 277-3552  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match 53.1%; Score 17; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4  
|||  
Db 2 FTVT 5

RESULT 7  
US-08-860-904-9  
Sequence 9, Application US/C8860904  
Patent No. 6294654  
GENERAL INFORMATION:  
APPLICANT: Sardie, Inger  
APPLICANT: Bogen, Bjarne  
APPLICANT: Fossum, Sigbjorn  
TITLE OF INVENTION: A Modified Immunoglobulin Molecule  
TITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR  
FILE REFERENCE: 9914-1  
CURRENT APPLICATION NUMBER: US/08/860,904  
EARLIER FILING DATE: 1997-09-29  
EARLIER APPLICATION NUMBER: PCT/GB96/00116  
EARLIER FILING DATE: 1996-01-19  
EARLIER APPLICATION NUMBER: GB 9501079.9  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Mus sp.

Query Match 50.0%; Score 16; DB 3; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7  
|||  
Db 1 TVSS 4

RESULT 8  
US-09-301-593-47  
Sequence 47, Application US/09301593A  
Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.189001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 47  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 50.0%; Score 16; DB 4; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7  
|||  
Db 1 TVSS 4

RESULT 9  
US-08-252-995D-7  
Sequence 7, Application US/08252995D  
Patent No. 5650501  
GENERAL INFORMATION:  
APPLICANT: Dennis, James W  
APPLICANT: Heffernan, Mike  
APPLICANT: Fode, Carol  
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BERESKIN & PARR  
STREET: 40 King Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/252,995D  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurdydyk, Linda M  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-08-252-995D-7  
Query Match 50.0%; Score 16; DB 1; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 7  
|||  
Db 2 LTLSN 6

RESULT 10  
US-08-478-386A-46  
Sequence 46, Application US/08478386A  
Patent No. 5830462  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,386A  
FILING DATE: 07/JUN/1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-478-386A-46

Query Match 50.0%; Score 16; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 6  
|||  
Db 3 LTVS 6

RESULT 11  
US-08-292-597-46

Sequence 46, Application US/08292597  
Patent No. 5834266  
GENERAL INFORMATION:  
APPLICANT: Gerald R. Crabtree  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: Regulated Apoptosis  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,597  
FILING DATE: 18/AUG/1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-108A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-292-597-46

Query Match 50.0%; Score 16; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 6  
|||  
Db 3 LTVS 6

RESULT 12  
US-08-388-653-46  
Sequence 46, Application US/08388653  
Patent No. 5869337  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/388,653
  FILING DATE: 14-FEB-1995
  CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/478,386
    FILING DATE: 07-JUN-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: Figg, E. Anthony
      REGISTRATION NUMBER: 27,295
      REFERENCE/DOCKET NUMBER: 2054-114A
    TELEPHONE: (202) 783-6040
    TELEFAX: (202) 783-6031
  INFORMATION FOR SEQ ID NO: 46:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 6 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
JS-08-388-653-46

Query Match: 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity: 75.0%; Pred. NO. 2.5e+05;
Matches: 3; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

CY 3 LTIS 6
DB 3 LTVS 6

RESULT 13
JS-08-473-985-46
Sequence 46, Application US/08473985
Patent No. 5871753
GENERAL INFORMATION:
  APPLICANT: Crabtree, Gerald R.
  APPLICANT: Schreiber, Stuart L.
  APPLICANT: Spencer, David M.
  APPLICANT: Wandless, Thomas J.
  APPLICANT: Belshaw, Peter
  APPLICANT: Ho, Steffan
  TITLE OF INVENTION: Regulated Transcription of Targeted Genes and
  TITLE OF INVENTION: Other Biological Events
  NUMBER OF SEQUENCES: 66
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Campbell and Flores
    STREET: 4370 La Jolla Village Drive, Suite 700
    CITY: San Diego
    STATE: California
    COUNTRY: USA
    ZIP: 92122
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent In Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/473,985
    FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/179,748
    FILING DATE: 07-JAN-1994
    ATTORNEY/AGENT INFORMATION:
      NAME: Campbell, Cathryn A.
      REGISTRATION NUMBER: 31,815
      REFERENCE/DOCKET NUMBER: P-SU 5863

```

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TELECOMMUNICATION INFORMATION:
  TELEPHONE: (619) 535-9001
  TELEFAX: (619) 535-8949
  INFORMATION FOR SEQ ID NO: 46:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 6 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-08-473-985-46

Query Match: 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity: 75.0%; Pred. NO. 2.5e+05;
Matches: 3; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

CY 3 LTIS 6
DB 3 LTVS 6

RESULT 14
US-08-934-108-7
Sequence 7, Application US/08934108
Patent No. 5976893
GENERAL INFORMATION:
  APPLICANT: Dennis, James W.
  APPLICANT: Heffernan, Mike
  APPLICANT: Fode, Carol
  TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BERESKIN & PARR
    STREET: 40 King Street West
    CITY: Toronto
    STATE: Ontario
    COUNTRY: Canada
    ZIP: M5H 3Y2
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent In Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/834,108
    FILING DATE:
  CLASSIFICATION: 536
  ATTORNEY/AGENT INFORMATION:
    NAME: Kurdydk, Linda M.
    REGISTRATION NUMBER: 34,971
    REFERENCE/DOCKET NUMBER: 3153-210
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (416) 364-7311
    TELEFAX: (416) 361-1398
  INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 6 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      ORIGINAL SOURCE:
        ORGANISM: Mus musculus
US-08-834-108-7

Query Match: 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity: 60.0%; Pred. NO. 2.5e+05;
Matches: 3; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

CY 3 LTIS 7
DB 2 LTLSN 6

```

RESULT 15  
 US-08-493-898-46  
 : Sequence 46, Application US/08483898  
 : Patent No. 5994313  
 : GENERAL INFORMATION:  
 : APPLICANT: Gerald R. Crabtree  
 : APPLICANT: Schreiber, Stuart J.  
 : APPLICANT: Spencer, David M.  
 : APPLICANT: Wandless, Thomas J.  
 : APPLICANT: Belshaw, Peter  
 : TITLE OF INVENTION: Regulated Apoptosis  
 : NUMBER OF SEQUENCES: 81  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
 : STREET: 26 Landsdowne Street  
 : CITY: Cambridge  
 : STATE: Massachusetts  
 : COUNTRY: USA  
 : ZIP: 02139  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC/DOS/MS/DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/483,898  
 : FILING DATE: 07-JUN-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/292,597  
 : FILING DATE: 18-AUG-1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Figg, E. Anthony  
 : REGISTRATION NUMBER: 27,195  
 : REFERENCE/DOCKET NUMBER: 2054-108A  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (202) 783-6040  
 : TELEFAX: (202) 783-6031  
 : INFORMATION FOR SEQ ID NO: 46:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-483-898-46

Query Match 50.0%; Score 16; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 6  
 Db 3 LTVS 6

Search completed: October 4, 2003, 12:50:33  
 Job time : 18 secs

GenCore version 5.1.5  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:52 ; Search time 19.3333 Seconds  
(without alignments)  
34.920 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLT: 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 293308 seqs, 96158652 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 3  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 761\*  
1: pir1\*  
2: pir2\*  
3: pir3\*  
4: pir4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	37.1	6	2 PD0028	pev-kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment)
2	12	34.3	5	2 A32516	cholecystokinin-5 - dog
3	12	34.3	5	2 PT0644	T-cell receptor be
4	12	34.3	7	2 B39127	phosphotransferase
5	12	34.3	7	2 PT0665	T-cell receptor be
6	11	31.4	7	2 I40697	biotin A - Citrob
7	11	31.4	7	2 E30608	Ig kappa chain V-I
8	10	28.6	6	2 PT0650	T-cell receptor be
9	10	28.6	7	2 S09066	globulin IV alpha
10	9	25.7	3	3 T13892	cytochrome-c oxida
11	9	25.7	5	2 E42364	flagellar protein
12	9	25.7	5	2 E60274	major protein anti
13	9	25.7	5	2 S68326	blood cell protein
14	9	25.7	5	2 S69237	surface protein te
15	9	25.7	6	2 A60986	N-formyl oligopept
16	9	25.7	6	2 B44510	hypothetical prote
17	9	25.7	6	2 A43766	28K ubiquitin-immu
18	9	25.7	6	2 I37263	Y protein - human
19	9	25.7	6	2 I65546	MHC H2-L antigen -
20	9	25.7	6	2 PT0587	T-cell receptor be
21	9	25.7	6	2 S29881	Na+/K+-exchanging
22	9	25.7	7	2 S25266	p1E protein - Esc
23	9	25.7	7	2 A25269	sex pheromone cM3
24	9	25.7	7	2 A30612	sex pheromone cCFL
25	9	25.7	7	2 PT0611	T-cell receptor be
26	8	22.9	4	2 PT0697	T-cell receptor be
27	8	22.9	5	2 I39964	ribosomal protein
28	8	22.9	5	2 I39966	ribosomal protein
29	8	22.9	5	2 I39965	ribosomal protein

30	8	22.9	5	2 A44692	fulicin - giant Af
31	8	22.9	5	2 PT0729	T-cell receptor be
32	8	22.9	5	2 PT0590	T-cell receptor be
33	8	22.9	5	2 G44817	27.5 kda structura
34	8	22.9	5	2 I44817	27.5K structural p
35	8	22.9	5	2 E44817	27.5K structural p
36	8	22.9	5	2 C44817	28.5K structural p
37	8	22.9	5	2 A44817	28K structural pro
38	8	22.9	5	3 CT0870	phytoosulfofokine alp
39	8	22.9	6	2 A13780	transferrin - bovi
40	8	22.9	6	2 A46474	Fc epsilon RI-b -
41	8	22.9	6	2 PT0637	T-cell receptor be
42	8	22.9	6	2 PT0641	T-cell receptor be
43	8	22.9	7	2 E61491	seed protein ws-5
44	8	22.9	7	2 PS0254	18K protein 5507 -
45	8	22.9	7	2 PT0642	T-cell receptor be

ALIGNMENTS

RESULT 1  
PD0028  
pev-kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment)  
C:Species: Penaeus vannamei  
C>Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 19-May-2000  
C:Accession: PD0028  
R:Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devree;  
Biochem. Biophys. Res. Commun. 248, 406-411, 1998  
A:Title: Identification of one tachykinin- and two kinin-related peptides in the brain  
A:Reference number: PD0027; MUID:98342103; PMID:9675150  
A:Accession: PD0028  
A:Molecule type: protein  
A:Residues: 1-6 <NIE>  
C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 37.1%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4  
|||  
DB 1 DFS 3

RESULT 2  
A32516  
cholecystokinin-5 - dog  
N:Alternate names: CCK-5  
C:Species: Canis lupus familiaris (dog)  
C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A32516  
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J  
Am. J. Physiol. 252, G272-G275, 1987  
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and int  
A:Reference number: A32516; MUID:87153871; PMID:3826354  
A:Accession: A32516  
A:Molecule type: protein  
A:Residues: 1-5 <SHI>  
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide  
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3  
||  
DB 4 DF 5

```
RESULT 3
PT0644
T-cell receptor beta chain V-D-J region (111-13) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0644
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0644
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-5 <PEE>
A/Experimental source: newborn thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      1 TDFT 4
      : ||
Db      2 SSFT 5

RESULT 4
B39127
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C/Accession: B39127
R/Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A/Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc
rin.
A/Reference number: A39127; MUID:91100329; PMID:1846143
A/Accession: B39127
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-7 <HAR>
A/Cross-references: GB:M38416; NID:G155142; PIDN:AAA98418.1; PID:G155144
C/Keywords: phosphotransferase

Query Match      34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 DF 3
      : |
Db      2 DF 3

RESULT 5
PT0665
T-cell receptor beta chain V-D-J region (121-35M) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0665
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0665
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-7 <PEE>
A/Experimental source: day 4 postnatal thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 DF 3
      : |
Db      2 DF 3

RESULT 6
I40697
biotin A - Citrobacter freundii (fragment)
C/Species: Citrobacter freundii
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C/Accession: I40697
R/Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A/Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobac
A/Reference number: I40697; MUID:89006280; PMID:2971595
A/Accession: I40697
A/Status: preliminary; translated from GB/EMBL/DDSM
A/Molecule type: DNA
A/Residues: 1-4 <RES>
A/Cross-references: GB:M21922; NID:G144434

Query Match      31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 TD 2
      : ||
Db      2 TD 3

RESULT 7
E30608
Ig kappa chain V-III region (Gag) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C/Accession: E30608
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S.
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A/Reference number: A30601; MUID:89215279; PMID:2496163
A/Accession: E30608
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <GON>
C/Keywords: heterotetramer; immunoglobulin

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      2 DFTLT 6
      : |
Db      1 EIVLT 5

RESULT 8
PT0650
T-cell receptor beta chain V-D-J region (121-3BP) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0650
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0650
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-6 <FEE>
A/Experimental source: day 4 postnatal thymus, strain BALB/c
C/Keywords: T-cell receptor
```

Query Match 28.6%; Score 10; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TFFT 4  
|||  
Db 3 SDAT 6

RESULT 9  
SC9066  
globulin IV alpha subunit delta-1 chain, seed - cucurbit (fragments)  
N;Alternate names: 11S globulin alpha subunit delta-1 chain  
C;Species: Cucurbita sp. (cucurbit)  
C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 38-Nov-1996  
C;Accession: S09066  
R;Ohmiya, M.; Hara, I.; Matsubara, H.  
Plant Cell. Physiol. 21, 157-167, 1980  
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and  
A;Reference number: SC9066  
A;Accession: SC9066  
A;Molecule type: protein  
A;Residues: 1-6;7 <OHM>

Query Match 28.6%; Score 10; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DFTL 5  
|||  
Db 3 DETI 6

RESULT 10  
T13892  
cytochrome-c oxidase (EC 1.9.3.1) chain I (imported) - river lamprey mitochondrion (frag  
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: T13892  
R;Delarbre, C.; Barriel, V.; Tillier, S.; Canver, P.; Gachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI  
A;Reference number: Z17775; MUID:97398704; PMID:9254918  
A;Accession: T13892  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <DEL>  
A;Cross-references: EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 25.7%; Score 9; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5  
|||  
Db 2 TL 3

RESULT 11  
E42364  
flagellar protein flrR - Salmonella typhimurium (fragment)  
C;Species: Salmonella typhimurium  
C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
C;Accession: E42364  
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991  
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq  
A;Reference number: A42364; MUID:91258342; PMID:1646201  
A;Accession: E42364

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <VOG>  
A;Cross-references: GB:M62408

Query Match 25.7%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5  
|||  
Db 3 TL 4

RESULT 12  
E60274  
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
C;Species: Mycobacterium tuberculosis  
C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
C;Accession: E60274  
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
Infect. Immun. 59, 372-382, 1991  
A;Title: Isolation and partial characterization of major protein antigens in the cultu  
A;Reference number: A60274; MUID:91099989; PMID:1898999  
A;Accession: E60274  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <NAG>

Query Match 25.7%; Score 9; DB 2; Length 5;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTLT 6  
|||  
Db 2 YPIT 5

RESULT 13  
S68326  
blood cell protein B - Ascidia ceratodes (fragment)  
N;Alternate names: Abcp-B  
C;Species: Ascidia ceratodes  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jun-1999  
C;Accession: S68326  
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.  
Arch. Biochem. Biophys. 324, 228-240, 1995  
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from  
A;Reference number: S68325; MUID:96132650; PMID:8554314  
A;Accession: S68326  
A;Molecule type: protein  
A;Residues: 1-5 <TAY>  
F;2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental  
F;4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 25.7%; Score 9; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3  
|||  
Db 2 DY 2

RESULT 14  
S69237  
surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)  
C;Species: Staphylothermus marinus  
C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: S69237  
R;Peters, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Eng  
J. Mol. Biol. 245, 385-401, 1995  
A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unu

A:Reference number: S69237; MUID:95139068; PMID:7817271  
A:Accession: S69237  
A:Molecule type: protein  
A:Residues: 1-5 <PEP>  
A:Experimental source: strain F1, DSM 1639  
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 25.7%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TIL 5  
Db 2 TIL 3

RESULT 15  
A60986  
N-formyl oligopeptide - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C:Accession: A60986  
R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.  
Experientia 45, 1097-1099, 1989  
A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl  
A:Reference number: A60986; MUID:90092408; PMID:2689204  
A:Accession: A60986  
A:Molecule type: protein  
A:Residues: 1-6 <BRO>  
C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.  
P:1/Modified site: N-formylmethionine #status experimental

Query Match 25.7%; Score 9; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
Db 3 FTL 5

Search completed: October 4, 2003, 12:49:37  
Job time : 20.3333 secs



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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:27:32 ; Search time 10 Seconds  
(without alignments)  
32.919 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.0

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	40.0	7	1 ALL7_CYPDPO	P82158 Cydia pomonella
2	12	34.3	5	1 RE11_LITRU	P82070 Litoria rubella
3	11	31.4	5	1 BIOA_CITFR	P13071 Citrobacter
4	11	31.4	5	1 RE31_LITRU	P82072 Litoria rubella
5	11	31.4	5	1 RE32_LITRU	P82073 Litoria rubella
6	10	28.6	5	1 E104_LITRU	P82100 Litoria rubella
7	9	25.7	7	1 CCF1_ENTFA	P20134 enterococcus
8	9	25.7	7	1 CIA_ENTFA	P11932 enterococcus
9	8	22.9	5	1 AL14_CARMA	P81817 carcinus ma
10	8	22.9	5	1 PSK_DAUCA	P58261 daucus caro
11	8	22.9	5	1 RE21_LITRU	P82071 Litoria rubella
12	8	22.9	7	1 ALL2_CARMA	P81805 carcinus ma
13	8	22.9	7	1 ALL3_CARMA	P81806 carcinus ma
14	8	22.9	7	1 ALL4_CARMA	P81807 carcinus ma
15	8	22.9	7	1 ALL5_CARMA	P81808 carcinus ma
16	8	22.9	7	1 FAR1_ASCSU	P31889 ascaris suu
17	7	20.0	4	1 RM01_YEAST	P36515 saccharomyc
18	7	20.0	6	1 FARP_MONEX	P41966 moniezia ex
19	7	20.0	6	1 LOK1_EOCMI	P41491 locusta mig
20	7	20.0	6	1 UN06_CLOPA	P81351 clostridium
21	7	20.0	7	1 FAR1_MACRS	P83274 macrobrachi
22	7	20.0	7	1 FAR1_PROCL	P38493 procambatus
23	7	20.0	7	1 FAR2_PROCL	P38498 procambatus
24	7	20.0	7	1 FAR4_PANRE	P41875 panagrellus
25	7	20.0	7	1 FARP_CALVO	P41866 calliphora
26	7	20.0	7	1 GFRP_MOUSE	P99025 mus musculu
27	7	20.0	7	1 IGAO_DCADE	P06294 dactylium d
28	6	17.1	3	1 LUXE_VIBFI	P24272 vibrio fisc
29	6	17.1	4	1 ACH1_ACHFU	P35904 achatina fu
30	6	17.1	4	1 FAR3_HIRME	P42562 hirudo medi
31	6	17.1	4	1 FAR4_HIRME	P42563 hirudo medi
32	6	17.1	4	1 FPKA_ANTEL	P58705 anthopleura
33	6	17.1	4	1 FLRF_HIRME	P42561 hirudo medi

34	6	17.1	4	1 FLRN_ANTEL	P58707 anthopleura
35	6	17.1	4	1 FMRP_VACNI	P01162 macrocallis
36	6	17.1	4	1 FYRI_ANTEL	P58706 anthopleura
37	6	17.1	4	1 OCP1_OCTMI	P58648 octopus min
38	6	17.1	4	1 OCP3_OCTMI	P58649 octopus min
39	6	17.1	5	1 E103_LITRU	P82099 litoria rub
40	6	17.1	5	1 FARP_ARITR	P41853 artiopesthi
41	6	17.1	5	1 PAP2_PARMA	P81864 pardachirus
42	6	17.1	5	1 SUGA_ACHDO	P19991 acheta dome
43	6	17.1	5	1 TPIS_CANFA	P54714 canis fami
44	6	17.1	5	1 TRM3_ECOLI	P13973 escherichia
45	6	17.1	5	1 UC22_MAIZE	P80628 zea mays (m

ALIGNMENTS

RESULT 1  
ALL7\_CYPDPO  
ID ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
CX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestruc J., Scott A.G., Kinstantley D.,  
Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily."  
RL Peptides 18:1301-1309(1997).  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 873 MW; 672879CABBS69350 CRC64;  
AMIDATION

Query Match 40.0%; Score 14; DB 1; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 1; indels 0; Gaps 0;

Oy 2 DFTL 5  
Db 4 DFGL 7

RESULT 2  
RE11\_LITRU  
ID RE11\_LITRU STANDARD; PRT; 5 AA.  
AC P82070;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 1.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
CX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella'. The skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";

RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

CC -!- MASS SPECTROMETRY: MW:598; METHOD=FAB.

KW Amphibian defense peptide.

SC SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DF 3

DB 2 DF 3

# RESULT 3

BIOA\_CITFR STANDARD; PRT; 5 AA.

ID BIOA\_CITFR

AC P13071;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Adenosyl-methionine-8-amino-7-oxononanoate aminotransferase

DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA

DE aminotransferase) (Fragment).

GN BIOA.

OS Citrobacter freundli.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

CC Enterobacteriaceae; Citrobacter.

OX NCBI\_TaxID=546;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8936280; PubMed=2971595;

RA Shiuan D., Campbell A.

RT "Transcriptional regulation and gene arrangement of *Escherichia coli*,

RT Citrobacter freundli and *Salmonella typhimurium* biotin operons."

RL Gene 67:203-211(1989).

CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-

CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-

CC diaminononanoate.

CC -!- COFACTOR: Pyridoxal phosphate.

CC -!- PATHWAY: Biotin biosynthesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent

CC aminotransferases.

CC -----

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

CC EMBL; M21922; ; NOT\_ANNOTATED\_CDS.

DR PIR; I40697; I40697.

DR InterPro; IPR005814; Aminotrans\_3.

DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.

KW Biotin biosynthesis; Transferase; Aminotransferase;

KW Pyridoxal phosphate.

FT NON\_TER 5

FT SEQUENCE 5 AA; 582 MW; 6AAAH1B1A6FC0000 CRC64;

Query Match

Best Local Similarity 31.4%; Score 11; DB 1; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TD 2

DB 3 TD 4

# RESULT 4

RE31\_LITRU

ID RE31\_LITRU STANDARD; PRT; 5 AA.

AC P82072;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Rubellidin 3.1.

OS Litoria rubella (Desert tree frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;

CC Pelodyadinae; Litoria.

OX NCBI\_TaxID=104895;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RA Steinbörner S.T., Wabnitz P.A., Waugh R.C., Bowie J.H., Gao C.,

RA Tyler M.J., Wallace J.C.

RT "The structure of new peptides from the Australian red tree frog

RT 'Litoria rubella'. The skin peptide profile as a probe for the study

RT of evolutionary trends of amphibians."

RL Aust. J. Chem. 49:955-963(1996).

CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic

CC activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.

KW Amphibian defense peptide; Amidation.

FT MOD\_RES 5 5 AMIDATION.

FT SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match

Best Local Similarity 31.4%; Score 11; DB 1; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 FT 4

DB 4 FT 5

# RESULT 5

RE32\_LITRU

ID RE32\_LITRU STANDARD; PRT; 5 AA.

AC P82073;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Rubellidin 3.2.

OS Litoria rubella (Desert tree frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;

CC Pelodyadinae; Litoria.

OX NCBI\_TaxID=104895;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.

RT "Peptides from the skin glands of the Australian buzzing tree frog

RT Litoria electrica. Comparison with the skin peptides from Litoria

RT rubella."

RL Aust. J. Chem. 52:639-645(1999).

CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic

CC activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

KW Amphibian defense peptide.

FT SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match

Best Local Similarity 31.4%; Score 11; DB 1; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FT 4  
|  
Db 4 FT 5

## RESULT 6

E104\_LITRU STANDARD; PRT; 5 AA.  
ID E104\_LITRU  
AC P82100;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 4.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
CX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645 (1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 5  
SQ SEQUENCE 5 AA; 616 MW; 61F2D1AC59AC0300 CRC64;

Query Match 28.6%; Score 10; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTI 7  
|  
Db 2 ITV 4

## RESULT 7

CCFL\_ENTFA STANDARD; PRT; 7 AA.  
ID CCFL\_ENTFA  
AC P20104;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CCF10.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
CX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=89008313; PubMed=3139659;  
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino Y.,  
RA Adsit J.C., Dunny G.M., Suzuki A.;  
RT "Structure of ccf10, a peptide sex pheromone which induces  
conjugative transfer of the Streptococcus faecalis tetracycline  
resistance plasmid, pCF10.";  
RL J. Biol. Chem. 263:14574-14578 (1988).  
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
HEMOLYSIN PLASMID PCF10.  
CX PIR; A30812; A30812.  
KW Pheromone.  
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5

Db 3 TL 4  
|

## RESULT 8

CIA\_ENTFA STANDARD; PRT; 7 AA.  
ID CIA\_ENTFA  
AC P11332;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
CX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87005252; PubMed=3093276;  
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,  
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;  
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,  
CAM373.";  
RL FEBS Lett. 206:69-72 (1986).  
CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS  
HARBORING PAM373.  
CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR  
SPECIFICITY OF PHEROMONES TO PLASMIDS.  
CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.  
DR PIR; A25269; A25269.  
KW Pheromone.  
SQ SEQUENCE 7 AA; 734 MW; 75BD572059C05D80 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
|  
Db 3 FIL 5

## RESULT 9

ALI4\_CARMA STANDARD; PRT; 5 AA.  
ID ALI4\_CARMA  
AC P81817;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 14.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734 (1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 5  
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
| |  
Db 3 FGL 5

RESULT 10  
PSK DAUCA STANDARD; PRT; 5 AA.  
AC P58261;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phytosulfokine-alpha (PSK-alpha) (Contains: Phytosulfokine-beta (PSK-beta)).  
DE Daucus carota (Carrot).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Campanulids; Apiales; Apiaceae; Daucus.  
OX NCBI\_TaxID=4039;  
RN [1]  
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
RC STRAIN=cv. JS-Harumakigosun;  
RX MEDLINE=20212743; PubMed=10750705;  
RA Hanai H., Matsuno T., Yamamoto Y., Matsubayashi Y., Kobayashi T.,  
RA Kanada H., Sakagami Y.;  
RT "A secreted peptide growth factor, phytosulfokine, acting as a  
RT stimulatory factor of carrot somatic embryo formation.";  
RL Plant Cell Physiol. 41:27-32(2000).  
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
CC EMBRYOS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
KW Growth factor; Sulfation.  
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.  
FT MOD\_RES 1 1 SULFATION.  
FT MOD\_RES 3 3 SULFATION.  
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B3C0000 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FT 4  
| |  
Db 3 YT 4

RESULT 11  
RE21 LITRU STANDARD; PRT; 5 AA.  
AC P82071;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.M., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic

CC activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAE.  
KW Amphibian defense peptide.  
SQ SEQUENCE 5 AA; 626 MW; 6ED9C9CB1C3C0000 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3  
| |  
Db 2 EF 3

RESULT 12  
ALL2 CARMA STANDARD; PRT; 7 AA.  
ID ALL2 CARMA  
AC P81805;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 2.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD\_RES 7 7 AMIDATION (POTENTIAL).  
SQ SEQUENCE 7 AA; 770 MW; 672679CDCB5DB70 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
| |  
Db 5 FGL 7

RESULT 13  
ALL3 CARMA STANDARD; PRT; 7 AA.  
ID ALL3 CARMA  
AC P81806;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 3.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the

T allatostatin superfamily in the shore crab Carcinus maenas.";  
L Eur. J. Biochem. 250:727-734(1997).  
C -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
C -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
Db 5 FGL 7

RESULT 14  
ALL4\_CARMA STANDARD; PRT; 7 AA.  
C P81807;  
T 30-MAY-2000 (Rel. 39, Created)  
T 30-MAY-2000 (Rel. 39, Last sequence update)  
T 30-MAY-2000 (Rel. 39, Last annotation update)  
E Carcinustatin 4.  
DS Carcinus maenas (Common shore crab) (Green crab).  
C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
C Eumalacostraca; Eucarida; Decapoda; Ploccymata; Brachyura;  
C Eubrachyura; Portunoidea; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
-N [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
TC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
Db 5 FGL 7

RESULT 15  
ALL5\_CARMA STANDARD; PRT; 7 AA.  
C P81808;  
T 30-MAY-2000 (Rel. 39, Created)  
T 30-MAY-2000 (Rel. 39, Last sequence update)  
T 30-MAY-2000 (Rel. 39, Last annotation update)  
E Carcinustatin 5.  
DS Carcinus maenas (Common shore crab) (Green crab).  
C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
C Eumalacostraca; Eucarida; Decapoda; Ploccymata; Brachyura;  
C Eubrachyura; Portunoidea; Portunidae; Carcinus.  
CX NCBI\_TaxID=6759;  
-N [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";

RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5  
Db 5 FGL 7

Search completed: October 4, 2003, 12:46:01  
Job time : 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 ; Search time 48 Seconds  
(without alignments)  
37.633 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTRMBL23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mtc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_virus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	31.4	7	2	Q54248 streptomyce
2	10	28.6	7	2	O34028 sphingomona
3	9	25.7	7	2	O07354 synechococc
4	9	25.7	7	10	P82445 nicotiana t
5	9	25.7	7	15	Q8JE81 human immun
6	8	22.9	7	2	P70804 azctobacter
7	7	20.0	5	2	P83073 bacillus ce
8	7	20.0	7	2	Q47029 enterobacte
9	7	20.0	7	2	P72081 nocardia la
10	7	20.0	7	8	C98866 spinacia ol
11	6	17.1	5	13	P83308 gallus gal-
12	6	17.1	6	10	P82541 spinacia ol
13	6	17.1	7	2	Q50556 actinobacil
14	6	17.1	7	2	Q8KMS9 enterobacte
15	6	17.1	7	4	Q15903 homo sapien
16	6	17.1	7	6	Q28742 oryctolagus

Q8mfy6 taraxacum i  
Q49223 glycine max  
Q9c5b3 arabidopsis  
Q8k3h6 rattus norv  
Q63480 rattus norv  
Q55184 rattus norv  
Q9YQ10 transmissib  
Q8JJ20 gallus gall  
P82181 spinacia ol  
P82182 spinacia ol  
Q8KMS3 klebsiella  
Q47505 escherichia  
Q95945 saccharomyc  
P93233 lycopersico  
Q67113 influenzavi  
Q65578 bovine hefp  
Q42564 fugu rubrip  
Q37624 rous sarcom  
Q38433 rattus sp.  
Q8G112 borrelia bu  
Q8G104 borrelia bu  
Q8G100 borrelia bu  
Q8nhh7 homo sapien  
Q15897 homo sapien  
P92214 amblyopyrum  
P92393 hordeum vul  
P92403 leptopyrum  
P92427 peridictyon  
Q99182 gnatholebia

ALIGNMENTS

RESULT 1  
Q54248  
ID Q54248 PRELIMINARY; PRT; 7 AA.  
AC Q54248;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RplO protein (Fragment).  
GN RPL0.  
OS Streptomyces griseus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1911;  
RN [1]  
RF SEQUENCE FROM N.A.  
RC STRAIN=N2-3-11;  
RX MEDLINE=20011291; PubMed=10542330;  
RA Poehling S., Piepersberg W., Wehmeier U.F.;  
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus  
N2-3-11 and interaction of the secY protein with the SecA protein.";  
RL Biochim. Biophys. Acta 1447:238-302(1999).  
DR EMBL; X95915; CAA65160.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2DiB2AC CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 8.3e-05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TLT 6  
Db 2 TVT 4

RESULT 2  
O34028  
ID O34028 PRELIMINARY; PRT; 7 AA.  
AC O34028;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Catechol-2,3-dioxygenase (Fragment).  
 GN PHNE.  
 OS *Sphingomonas chungbukensis*.  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
 CC Sphingomonadaceae; Sphingomonas.  
 CC NCBI\_TaxID=56193;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=DJ77;  
 RC Kim Y.-C.;  
 RA Submitted (FEB-1997) to the EXBL/GenBank/DBJ databases.  
 RL EMBL; J88298; AAB66311.1; -.  
 DR Dioxigenase.  
 KW NON\_TER  
 FT SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;  
 SQ  
 Query Match 28.6%; Score 10; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LTI 7  
 DB 3 MTV 5

RESULT 3  
 007354 PRELIMINARY; PRT; 7 AA.  
 ID 007354  
 AC 007354;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NifK (Fragment).  
 GN NIFK.  
 OS *Synechococcus* sp. (strain PCC 8801 / RP-1) (Cyanothecae PCC 8801).  
 CC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.  
 CC NCBI\_TaxID=41431;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=RF-1;  
 RC MEDLINE=99231861; PubMed=10217509;  
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;  
 RT "Organization and expression of nitrogen-fixation genes in the aerobic  
 RT nitrogen-fixing unicellular cyanobacterium *Synechococcus* sp. strain  
 RT RF-1.";  
 RL Microbiology 145:743-753(1999).  
 DR EMBL; AF003700; AAC35193.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;  
 Query Match 25.7%; Score 9; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 PTL 5  
 DB 3 PDL 5

RESULT 4  
 P82445 PRELIMINARY; PRT; 7 AA.  
 ID P82445  
 AC P82445;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 10 kDa cell wall protein (fragment).  
 OS *Nicotiana tabacum* (Common tobacco).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.

OX NCBI\_TaxID=4097;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL *Planta* 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 7  
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1B862D1B2A0 CRC64;  
 Query Match 25.7%; Score 9; DB 10; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LTI 7  
 DB 1 VTV 3

RESULT 5  
 08JEB1 PRELIMINARY; PRT; 7 AA.  
 ID 08JEB1  
 AC 08JEB1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN PCL.  
 OS Human immunodeficiency virus 1.  
 CC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 CC NCBI\_TaxID=11676;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=4874;  
 RC MEDLINE=22056123; PubMed=12060770;  
 RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
 RA Hoffmann D., Korn K., Selbig J.;  
 RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics  
 RT approach to predicting phenotype from genotype.";  
 RL *Proc. Natl. Acad. Sci. U.S.A.* 99:8271-8276(2002).  
 DR EMBL; AF347267; AAK32344.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;  
 Query Match 25.7%; Score 9; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TL 5  
 DB 4 TL 5

RESULT 6  
 P708C4 PRELIMINARY; PRT; 7 AA.  
 ID P708C4  
 AC P708C4;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Algt protein (Fragment).  
 GN ALGT.  
 OS *Azotobacter vinelandii*.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Azotobacter.  
 CC NCBI\_TaxID=354;  
 RN (1)  
 RN SEQUENCE FROM N.A..

RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=9930682;  
RA Rehm B.H.A., Ertesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
part of an alg gene cluster physically organized in a manner similar  
to that in Pseudomonas aeruginosa";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 22.9%; Score 8; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TI 7  
|:  
Db 2 TV 3

RESULT 7  
P83073  
ID P83073 PRELIMINARY; PRT; 5 AA.  
AC P83073;  
DT 01-OCT-2001 (TReMBLrel. 18, Created);  
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update);  
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update);  
DE 88 kDa protein (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NCIMB 11796;  
RA Browne N., Dowds R.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA; 623 MW; 6BC1AAA336F00000 CRC64;

Query Match 20.0%; Score 7; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TD 2  
|:  
Db 4 TE 5

RESULT 8  
Q47029  
ID Q47029 PRELIMINARY; PRT; 7 AA.  
AC Q47029;  
DT 01-NOV-1996 (TReMBLrel. 01, Created);  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update);  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update);  
DE Aad A1 protein (Fragment).  
GN AAD A1.  
OS Enterobacter cloacae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=550;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94079349; PubMed=8257126;  
RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.C.;  
RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-  
acetyltransferase";  
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).  
DR EMBL; M88012; AAA16193.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 20.0%; Score 7; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 LT 6  
|:  
Db 1 IT 2

RESULT 9  
P72081  
ID P72081 PRELIMINARY; PRT; 7 AA.  
AC P72081;  
DT 01-FEB-1997 (TReMBLrel. 02, Created);  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update);  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update);  
DE 3'-methylcephem hydroxylase (Fragment).  
GN CEF3.  
OS Nocardia lactamdurans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.  
OX NCBI\_TaxID=1913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96009872; PubMed=7557411;  
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.J., Martin J.F.,  
RA Liras P.;  
RT "Characterization of the cmcH genes of Nocardia lactamdurans and  
Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem  
O-carbamoyltransferase for cephamycin biosynthesis";  
RL Gene 162:21-27(1995).  
DR EMBL; Z21682; CAA79797.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDE1E631C0 CRC64;

Query Match 20.0%; Score 7; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5  
|:  
Db 1 TM 2

RESULT 10  
O98866  
ID O98866 PRELIMINARY; PRT; 7 AA.  
AC O98866;  
DT 01-MAY-1999 (TReMBLrel. 10, Created);  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update);  
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update);  
DE Cytochrome b/f subunit IV (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86120353; PubMed=3003688;  
RA Sijben-Mueller G., Hallick R.B., Ait J., Westhoff P., Herrmann R.G.;  
RT "Spirach plastid genes coding for initiation factor IF-1, ribosomal  
protein S11 and RNA polymerase alpha-subunit";  
RL Nucleic Acids Res. 14:1029-1044(1986).  
DR EMBL; X03496; CAA27215.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 20.0%; Score 7; DB 8; Length 7;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Qy 2 DF 3  
1 NF 2

## RESULT 11

P83308  
ID P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE FMRamide-like neuropeptide (LPLRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RX PubMed=613771;  
RA Dockray G.J., Reeve J.R. Jr., Shavey J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by  
RT antibodies to FMRamide."  
RL Nature 305:328-330(1983).  
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE FMRP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 17.1%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 F 3  
1  
5 F 5

## RESULT 12

P82541  
ID P82541 PRELIMINARY; PRT; 6 AA.  
AC P82541;  
DT 01-OCT-2003 (TrEMBLrel. 15, Created)  
DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).  
OS Spinacia oleracea (Spinach).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC STRAIN=cv. ALVARO; TISSUE=Leaf;  
RX MEDLINE=20435797; PubMed=10874039;  
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
RT "The plastid ribosomal proteins. Identification of all the proteins in  
RT the small subunit of an organelle ribosome (chloroplast)."  
RL J. Biol. Chem. 37:28455-28465(2000).  
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.  
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.  
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA  
CC FORM IS THE MINOR BASIC FORM.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.  
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
DR InterPro; IPR002222; Ribosomal\_S19.

DR Pfam; PF00203; Ribosomal\_S19; PARTIAL.  
DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; PARTIAL.  
KW Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 17.1%; Score 6; DB 10; Length 6;  
Best Local Similarity 25.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TLTI 7  
1 TRSL 4

## RESULT 13

O52556  
ID O52556 PRELIMINARY; PRT; 7 AA.  
AC O52556;  
DT 01-JUN-1999 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE GLYA (Fragment).  
GN GLYA.  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
OS actinomycetemcomitans).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33384;  
RX MEDLINE=96355846; PubMed=8751884;  
RA Kolodrubetz D., Spitznagel E. Jr., Wang R., Phillips L.H., Jacobs C.,  
RA Kraig E.;  
RT "cis Elements and trans factors are both important in strain-specific  
RT regulation of the leukotoxin gene in Actinobacillus  
RT actinomycetemcomitans."  
RJ Infect. Immun. 64:3451-3460(1996).  
DR EMBL; U51862; AAB88721.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 17.1%; Score 6; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTI 7  
3 LPIV 5

## RESULT 14

Q8KMS9  
ID Q8KMS9 PRELIMINARY; PRT; 7 AA.  
AC Q8KMS9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN TNIA.  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=143777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CH2-4;  
RX MEDLINE=21604134; PubMed=11763242;  
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Mirakhina S.V.,  
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova N.A.,  
RA Yurieva O.V., Nikiforov V.G.;

RT "Mercury resistance transposons of Gram-negative environmental  
bacteria and their classification."  
Res. Microbiol. 152:811-822(2001).  
OR EMBL; AJ302778; CAC83058.1; --  
FT NON\_TER  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DA9AC CRC64;

Query Match 17.1%; Score 6; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 F 3  
|  
Db 1 F 1

RESULT 15

Q15903 PRELIMINARY; PRT; 7 AA.  
ID Q15903;  
AC Q15903;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE (Clone XP7E7B) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN 1;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32082; AAA73933.1; --  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 7 AA; 949 MW; 6B040339CDD33BDC CRC64;

Query Match 17.1%; Score 6; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 F 3  
|  
Db 4 F 4

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:26:27 ; Search time 51.6667 Seconds  
(without alignments:  
21.505 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFLT7 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 76613

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	85.7	7	20 AAY40738	S4 derivative #12,
2	30	85.7	7	2: AAB30076	Scaffold protein S
3	27	77.1	7	20 AAY40737	S4 derivative #11,
4	27	77.1	7	21 AAB30075	Scaffold protein S
5	26	74.3	7	20 AAY40736	S4 derivative #10,
6	26	74.3	7	21 AAB30074	Scaffold protein S
7	21	60.0	7	20 AAY14399	Peptide CDR-H1-7(Y
8	20	57.1	5	23 AAU85454	Human colon specif
9	20	57.1	6	19 AAW31467	Transcriptional ac

10	19	54.3	5	9 AAP82200	Example of peptide
11	19	54.3	6	20 AAY06466	Epitope tag, Synt
12	19	54.3	6	21 AAY77708	AUS peptide epitop
13	19	54.3	6	22 AAE13076	Epitope tag #4 use
14	19	54.3	6	22 AAY51422	Integrin activatin
15	19	54.3	6	22 AAB97355	AUS epitope used i
16	19	54.3	6	22 AAB59859	AUS peptide epitop
17	19	54.3	6	23 ABG32853	Epitope tag for ye
18	19	54.3	6	23 AAE24857	AUS peptide used i
19	19	54.3	6	23 AAE16558	Epitope tag #2 fus
20	19	54.3	7	21 AAY52584	Amaranthus viridis
21	18	51.4	6	19 AAW75358	Hexapeptide #13 bi
22	18	51.4	6	19 AAW75292	Hexapeptide #13 bi
23	18	51.4	7	11 AAR09409	IFA-1 alpha subuni
24	18	51.4	7	19 AAW58711	Tryptic 40 kD subu
25	18	51.4	7	20 AAY14403	Peptide CDR-H1-7 d
26	18	51.4	7	22 AAG64484	Antih hepatitis C pe
27	17	48.6	4	23 ABB55625	Mutated protein ki
28	17	48.6	4	23 ABB55651	Mutated protein EG
29	17	48.6	5	21 AAB52195	Human anti-HBs ant
30	17	48.6	5	21 AAB17215	IS-1 antagonist pe
31	17	48.6	5	21 AAY51466	AAV VP3 derived pe
32	17	48.6	5	23 ABB72462	Interleukin 1 anta
33	17	48.6	5	24 ABJ12234	Streptococcal prot
34	17	48.6	5	24 ABU12235	Streptococcal prot
35	17	48.6	6	20 AAY33711	Hepatoma diagnosti
36	17	48.6	6	20 AAY06532	Epidermal growth f
37	17	48.6	6	21 AAY95393	Human pancreatic p
38	17	48.6	6	22 AAG98217	Human SNP associat
39	17	48.6	6	22 AAB87699	Hepatoma-diagnosti
40	17	48.6	6	22 AAB55567	T cell surface rec
41	17	48.6	6	22 AAB57414	CD90 C-terminal co
42	17	48.6	6	22 AAB57824	CD90 C-terminal co
43	17	48.6	6	23 AAC19357	Alpha4beta7-integr
44	17	48.6	6	23 ABJ05046	T-cell surface rec
45	17	48.6	6	23 ABP63294	T cell surface rec

ALIGNMENTS

RESULT 1  
AAY40738  
10 AAY40738 standard; peptide; 7 AA.  
XX  
AC AAY40738;  
XX  
DT 01-DEC-1999 (first entry)  
XX  
DE S4 derivative #12, beta strand of scaffold protein structure.  
XX  
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
KW tumour; chemotherapeutic agent.  
XX  
CS Synthetic.  
XX  
EN EP947582-A1.  
XX  
FD 06-OCT-1999.  
XX  
PF 31-MAR-1998; 98EP-0870065.  
XX  
PR 31-MAR-1998; 98EP-0870065.  
XX  
(INNO-) INNOGENETICS NV.  
Desmet J, Hufton S, Hoogenboom H, Sablon E;  
WPI; 1999-542958/46.  
XX  
PT New scaffold protein, useful for stabilizing antigens used as vaccines  
XX

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a

CC cytotoxic molecule or an autoimmune antibody which may then kill the

CC tumour cells. Therefore the scaffold protein may be used to target

CC chemotherapeutic agents to specific cells. It may also be used to

CC stabilize individual peptides in a peptide library and may be used in

CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX

SQ Sequence 7 AA;

Query Match 85.7%; Score 30; D3 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7

Db 1 DFTLTI 6

RESULT 2

AAB30076

ID AAB30076 standard; Peptide: 7 AA.

XX

AC AAB30076;

XX

DT 09-FEB-2001 (first entry)

XX

DE Scaffold protein: SCA S4 peptide SEQ ID NO: 137.

XX

KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;

KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;

KW diabetic retinopathy; atherosclerosis.

XX

CS Synthetic.

XX

PN WC200060070-A1.

XX

PD 12-OCT-2000.

XX

PF 01-APR-1999; 99WC-EP02283.

XX

PR 01-APR-1999; 99WC-EPC2283.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX

DR WPI; 2000-665002/64.

XX

PT Scaffold composed of single-chain polypeptide having beta sandwich

PT architecture carrying new and randomized peptide sequences useful as

PT supporting framework and carrying antigen- or receptor binding

PT fragments

XX

PS Disclosure; Page 15; 68pp; English.

XX

CC The present invention is concerned with producing scaffold proteins

CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be

CC used as a scaffold to bind antigen- or receptor-binding fragments. These

CC can be used in the treatment of diseases such as cancer,

CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and

CC diabetic retinopathy. Sequences AAB29930-S29939 were used in the

CC production of the proteins of the invention.

XX

SQ Sequence 7 AA;

Query Match 85.7%; Score 30; D3 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7

Db 1 DFTLTI 6

RESULT 3

AAY40737

ID AAY40737 standard; peptide: 7 AA.

XX

AC AAY40737;

XX

DT 01-DEC-1999 (first entry)

XX

DE S4 derivative #11, beta strand of scaffold protein structure.

XX

KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;

KW tumour; chemotherapeutic agent.

XX

CS Synthetic.

XX

PN EP947582-A1.

XX

PD 06-OCT-1999.

XX

PF 31-MAR-1998; 98EP-0870065.

XX

PR 31-MAR-1998; 98EP-0870065.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX

DR WPI; 1999-542958/46.

XX

PT New scaffold protein, useful for stabilizing antigens used as vaccines

PT

XX

PS Disclosure; Page 6; 105pp; English.

XX

CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a  
CC cytotoxic molecule or an autoimmune antibody which may then kill the  
CC tumour cells. Therefore the scaffold protein may be used to target  
CC chemotherapeutic agents to specific cells. It may also be used to  
CC stabilize individual peptides in a peptide library and may be used in  
CC diagnostic techniques, and to stabilize antigens used as vaccines.  
XX

SQ Sequence 7 AA;

Query Match: 77.1%; Score 27; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7  
|:|:|  
Db 1 DYTJTI 6

RESULT 4

AAB30075  
ID AAB30075 standard; Peptide; 7 AA.

AC AAB30075;

DT 09-FEB-2001 (first entry)

DE Scaffold protein SCA S4 peptide SEQ ID NO: 136.

DE Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
KW diabetic retinopathy; atherosclerosis.  
XX

OS Synthetic.

PN WO20060070-A1.

PD 12-OCT-2000.

PF 01-APR-1999; 99WC-EP02283.

PR 01-APR-1999; 99WC-EP02283.

PA (INNO-) INNOGENETICS NV.

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

DR WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich  
PT architecture carrying new and randomized peptide sequences useful as  
PT supporting framework and carrying antigen- or receptor binding  
PT fragments -  
XX

PS Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins  
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be  
CC used as a scaffold to bind antigen- or receptor-binding fragments. These  
CC can be used in the treatment of diseases such as cancer,  
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and  
CC diabetic retinopathy. Sequences AAB29930-329939 were used in the  
CC production of the proteins of the invention.  
XX

SQ Sequence 7 AA;

Query Match: 77.1%; Score 27; DB 21; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7  
|:|:|  
Db 1 DYTJTI 6

RESULT 5

AAY40736

ID AAY40736 standard; peptide; 7 AA.

XX AAY40736;

DT 01-DEC-1999 (first entry)

DE S4 derivative #10, beta strand of scaffold protein structure.

KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
KW tumour; chemotherapeutic agent.  
XX

OS Synthetic.

EN EP947582-A1.

PD 06-OCT-1999.

PF 31-MAR-1998; 98EP-0870065.

PR 31-MAR-1998; 98EP-0870065.

PA (INNO-) INNOGENETICS NV.

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

DR WPI; 1999-542958/46.

PT New scaffold protein, useful for stabilizing antigens used as vaccines  
PT -  
XX

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the  
CC S4 peptide (AAY40607) which forms part of a beta sheet. Peptides  
CC beta strand peptide which forms part of a beta sheet. Peptides  
CC (AAY40601-Y40609) together form a single-chain scaffold protein which  
CC contains at least 1 disulfide bond, contains less than 10% alpha helix  
CC and contains at least 6 beta-strands. The scaffold protein is constructed  
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any  
CC functionally equivalent derivative of these sequences. The beta strands  
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to  
CC the next by hydrogen bonds, which generate a beta sandwich architecture.  
CC If the additional beta strands A1-A3 are included in the structure the  
CC scaffold is constructed of two beta sheets, with the structures  
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each  
CC other via amino acid loops, where at least one of the loops binds to a  
CC receptor or antigen. The scaffold protein is used to stabilize antigens  
CC or whole proteins such as receptors, or their fragments. It may be used  
CC to bind two separate molecules. For example, one surface of the scaffold  
CC may be bound to a protein which binds to a tumour antigen. This will  
CC target the complex to tumour cells. Another surface may be bound to a  
CC cytotoxic molecule or an autoimmune antibody which may then kill the  
CC tumour cells. Therefore the scaffold protein may be used to target  
CC chemotherapeutic agents to specific cells. It may also be used to  
CC stabilize individual peptides in a peptide library and may be used in  
CC diagnostic techniques, and to stabilize antigens used as vaccines.  
XX

SQ Sequence 7 AA;

Query Match: 74.3%; Score 26; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7  
|:|:|  
Db 1 DFTLSI 6

RESULT 6

AAB30074

```
ID AAB30074 standard; Peptide; 7 AA.
XX
AC AAB30074;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
XX
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WC-EP02283.
XX
PR 01-APR-1999; 99WC-EP02283.
XX
PA (INNO-) INNOGENETICS NV.
PI Desmet J, Hufton S, Hoogenboom H, Sablon B;
XX
DR WPI; 2000-665002/64.
XX
PT Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments.
XX
PS Disclosure; Page 15; 58pp; English.
XX
CC The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB29930-B29939 were used in the
CC production of the proteins of the invention.
XX
SQ Sequence 7 AA;
Query Match 74.3%; Score 26; DB 21; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 3; Gaps 3;
QY 2 DFTLT: 7
DB 1 DFTLS: 6
RESULT 7
AAY14399
ID AAY14399 standard; peptide; 7 AA.
XX
AC AAY14399;
XX
DT 17-AUG-1999 (first entry)
XX
DE Peptide CDR-H1-7(Y3F) derived from anti-HCV protease MAb 8D4.
XX
KW Complementarity determining region; CDR; monoclonal antibody; MAb;
KW hepatitis C virus; HCV; protease; binding site.
XX
OS Synthetic.
XX
PN JP1:127861-A.
XX
PD 18-MAR-1999.
XX
```

```
PF 29-OCT-1997; 97JP-0297451.
XX
PR 29-OCT-1997; 97JP-0297451.
XX
PA (NIHA ) JAPAN ENERGY CORP.
XX
DR WPI; 1999-350322/30.
XX
KW Neutralized antibody partial peptide derived from hepatitis C virus
KW - useful for inhibiting Hepatitis C Virus (HCV) serine protease
KW activity
XX
PS Example 1; Page 24; 32pp; Japanese.
XX
CC This sequence corresponds to a peptide (CDR-H1-7; AAY14433) derived from
CC the sequence of the heavy chain variable region complementarity
CC determining region (CDR)-1 of the anti-hepatitis C virus (HCV) Ser/Thr
CC protease monoclonal antibody (MAb) 8D4 protein. The peptide has a Tyr
CC to Phe amino acid substitution at position 3 compared to the CDR-H1-7
CC peptide. The invention relates to the use of partial peptides
CC (AAY14348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease
CC activity.
XX
SQ Sequence 7 AA;
Query Match 60.0%; Score 21; DB 23; Length 7;
Best Local Similarity 80.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TDFTL: 5
DB 1 TDFVL: 5
RESULT 8
AAU85454
ID AAU85454 standard; Peptide; 5 AA.
XX
AC AAU85454;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human colon specific polypeptide antibody binding site #31.
XX
KW Human; colon specific gene; CSG; cytostatic; metastasis;
KW colon cancer staging; antibody binding site.
XX
OS Homo sapiens.
XX
PN WC200206515-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US22454.
XX
PR 17-JUL-2000; 2000US-0618596.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Sun Y;
XX
DR WPI; 2002-171815/22.
XX
PT Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient, and
PT comparing it with levels of the gene from a normal human control.
XX
PS Disclosure; Page 2; 52pp; English.
XX
CC The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific
```

CC gene (CSG) in cells, tissues or bodily fluids and comparing it with  
CC levels of CSG in cells, tissues or bodily fluids from a normal human  
CC control. Colon cancer can be treated by administering a molecule which  
CC down regulates the expression or activity of CSG. An immune response  
CC against a target cell expressing CSG can be induced by delivering an  
CC immunologically stimulatory amount of a CSG protein to a patient, so that  
CC an immune response is mounted. Therapeutic agents are useful for imaging  
CC colon cancer in a patient by administering an agent labelled with  
CC paramagnetic ions or a radioisotope to the patient. They are also useful  
CC for preventing the onset of colon cancer, and in diagnosis and treatment  
CC of the disease. Sequences AAU85424-AAU85502 represent human colon  
CC specific protein antibody binding sites used in the method of the  
CC invention.  
XX  
SQ

Query Match 57.1%; Score 20; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FTLL 6  
|||  
Db 2 FLL 5

RESULT 9  
AAW31467  
ID AAW31467 standard; Protein; 6 AA.

XX AAW31467;

XX 04-AUG-1996 (first entry)

DT Transcriptional activator peptide fragment LS130.

DE  
XX  
KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;  
KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;  
GW Gal1; DNA binding domain.

XX Synthetic.

OS WO9744447-A2.

XX 27-NOV-1997.

XX 02-MAY-1997; 97WO-US07338.

XX 01-MAY-1997; 97US-0017016.

XX 03-MAY-1996; 96JS-0017016.

XX (HARD) HARVARD COLLEGE.

XX Lu X, Ptashne M, Wu Y;

XX WPI; 1996-018502/02.

XX N-PSDB; AAV02565.

XX New transcriptional activator containing DNA binding domain. bound to  
PT peptide - useful for controlling gene expression, especially in gene  
PT therapy, and in protein-protein interaction assays, does not inhibit  
PT other transcription activators

XX Example 1; Page 26; 55pp; English.

XX AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076  
CC are fragments used in an assay to determine novel transcriptional  
CC activators. The method involves the production of transcriptional  
CC activators comprising of a DNA-binding group and a 6-25 amino acid  
CC peptide that is covalently bonded to the DNA binding group and does not  
CC represent a fragment of a natural transcription activator.

CC Protein-protein interactions are identified in the assay by fusing a  
CC DNA-binding domain to a library of DNA fragments and introducing this and  
CC a fusion of target protein and a polypeptide containing a region of Gal4

CC which interacts with GalLP into a cell containing GalLP and identifying  
CC members of the library that interact with the target from activation of  
CC transcription. Such constructs are used to activate transcription in a  
CC cell, e.g. for controlling gene activity, particularly in gene therapy  
CC (e.g. recognizing a site close to a selected therapeutic gene).  
CC Transcription can be activated without blocking other transcriptional  
CC activators. They probably act by interacting with a component of the RNA  
CC polymerase II holoenzyme, Gal1, the strongest known yeast activator,  
CC which provides a more sensitive assay allowing detection of even weak  
CC protein-protein interactions. Such activators do not create toxicity  
CC problems even when overexpressed.

XX Sequence 6 AA;

Query Match 57.1%; Score 20; DB 19; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDTLL 5  
|||  
Db 1 TDFLL 5

RESULT 10  
AAP82200

ID AAP82200 standard; protein; 5 AA.

XX AAP82200;

XX 25-OCT-1990 (first entry)

DE Example of peptide 2 for treatment of schizophrenia or psoriasis.

XX schizophrenia; psoriasis; vasoactive intestinal polypeptide.

XX synthetic.

XX SE8700125-A.

XX 16-JUL-1988.

XX 15-JAN-1987; 87SE-0000125.

XX 15-JAN-1987; 87SE-0000125.

XX (WERT) WETTERBERG.

XX Wetterberg J;

XX WPI; 1988-328337/46.

XX Short peptides for treatment of psoriasis and schizophrenia -  
PT comprise vasoactive intestinal polypeptide, peptide 7 or short  
PT peptide with five aminoacids

XX Claim 1; Page 5; 9pp; Swedish.

XX Specific example of pentapeptide of the general formula of AAP82197.  
CC These peptides can be administered intravenously,  
CC topically or perorally to relieve the symptoms of psoriasis or  
CC schizophrenia. Amino acids at posns 2 and 3 can be any residue but  
CC Asp is preferred at posn 3. See also AAP82196-9.

XX Sequence 5 AA;

Query Match 54.3%; Score 19; DB 9; Length 5;  
Best Local Similarity 75.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDTT 4  
|||  
Db 2 TDTT 5

```

RESULT 11
ID AAY06466 standard; peptide; 6 AA.
XX AC AAY06466;
XX DT 27-SEP-1999 (first entry)
XX DE Epitope tag.
XX KW Epitope tag; antibody engineering; yeast; surface display;
XX KW protein library; peptide library.
XX OS Synthetic.
XX PN WO9936569-A1.
XX PD 22-JUL-1999.
XX PF 20-JAN-1999; 99WO-US0118A.
XX PR 26-AUG-1998; 98US-0140094.
XX PR 20-JAN-1998; 98US-000938A.
XX PA (UNII ) UNIV ILLINOIS FOUND.
XX PI Boder ET, Kieke MC, Kranz DM, Shusta B, Witterup KD;
XX WP1; 1999-430619/36.
XX PT Selecting proteins with enhanced phenotypic properties than
XX PT wild-type proteins, is useful for high-y specific cancer diagnosis
XX PT and therapy
XX PS Disclosure; Page 7; 116pp; English.
XX CC This peptide comprises an epitope tag that can be used in
XX CC methods of the invention. The invention discloses a powerful new
XX CC system for engineering antibody affinity and specificity, by
XX CC constructing a microbial analogue of the mammalian system's B cell
XX CC repertoire. Antibodies are displayed on the surface of yeast cells
XX CC by genetic fusion with yeast cell wall proteins, especially
XX CC agglutinin proteins. After mutation, variants are selected on the
XX CC basis of improved binding characteristics with fluorescently
XX CC labeled targets. The selection method also identifies proteins
XX CC with enhanced phenotypic characteristics, proteins that are
XX CC displayed at higher levels, proteins that are secreted at higher
XX CC efficiency and proteins of improved stability.
XX SQ Sequence 6 AA;
XX Query Match 54.3%; Score 19; DB 20; Length 6;
XX Best Local Similarity 80.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFYL 5
Db 1 TDFYL 5

RESULT 12
ID AAY77708 standard; peptide; 6 AA.
XX AC AAY77708;
XX DT 12-MAY-2000 (first entry)
XX DE AJS peptide epitope.
XX KW Cell surface receptor; luminescence; protein internalization;
XX KW drug discovery; screening assay; epitope; AJS.
XX OS Synthetic.
XX PN WO200003246-A2.
XX PD 20-JAN-2000.
XX PF 13-JUL-1999; 99WO-US15870.
XX PR 13-JUL-1998; 98US-0092671.
XX PA (CELL-) CELLOMICS INC.
XX PI Rubin RA, Giuliano KA, Gough A, Dunlay T;
XX WP1; 2000-171170/15.
XX PT Automated screening method for identifying compounds which induce cell
XX PT surface receptor internalization, useful for drug discovery -
XX PS Example 6; Page 67; 148pp; English.
XX CC The invention relates to a method for identifying compounds which
XX CC inhibit internalization of cell surface receptors. Provided are an array
XX CC of locations, each containing cells with a cell surface receptor
XX CC protein, that are treated with a test compound. The protein is
XX CC luminescently labeled or contacted with a luminescently labeled cell
XX CC before or after test compound treatment. Any luminescence produced is
XX CC converted into digital data and automatically analysed to determine if
XX CC the test compound induced the protein internalization. The novel method
XX CC is used to screen for compounds which modulate cell surface receptor
XX CC protein internalization, this can be used in drug discovery, to test
XX CC compound efficacy in living biological systems. The assay method is
XX CC automated and compact. It has high throughput and uses smaller volumes of
XX CC reagents and test compounds. Sequences AAY77704-718 represent examples of
XX CC peptide epitope tags used in the course of the invention.
XX SQ Sequence 6 AA;
XX Query Match 54.3%; Score 19; DB 21; Length 6;
XX Best Local Similarity 80.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFYL 5
Db 1 TDFYL 5

RESULT 13
ID AAE13076 standard; peptide; 6 AA.
XX AC AAE13076;
XX DT 28-JAN-2002 (first entry)
XX DE Epitope tag #4 used in yeast cell surface display of proteins.
XX KW Phenotypic property; yeast; cell wall protein; epitope tag.
XX OS Unidentified.
XX PN US6300065-B1.
XX PD 09-OCT-2001.
XX PF 26-AUG-1998; 98US-0140094.
XX PR 31-MAY-1996; 96US-018741P.
XX PR 30-MAY-1997; 97US-0866398.
XX PR 20-JAN-1998; 98US-000938A.
XX PA (UNII ) UNIV ILLINOIS FOUND.
```



XX Kieke MC, Wattrup KD, Bader ET, Kranz DM, Shusta E;  
XX WPI; 2001-656236/75.  
XX  
XX Selecting proteins, e.g. antibodies, with enhanced phenotypic  
PT properties relative to those of a wild-type comprises transforming  
PT yeast cells with a vector expressing a protein to be tested fused to a  
PT yeast cell wall protein -  
XX  
XX Disclosure; Column 5; 64pp; English.  
PS  
XX  
XX The present invention relates to a method for selecting proteins with  
CC enhanced phenotypic properties relative to those of a wild-type,  
CC comprises transforming yeast cells with a vector expressing a protein  
CC to be tested fused to a yeast cell wall protein. The method is  
CC particularly useful for selecting antibodies for improved affinity and  
CC specificity. The present sequence is an epitope tag which is used in  
CC yeast cell surface display of proteins.  
XX  
SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 22; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
: |||  
Db 1 TDFYL 5

RESULT 14  
AAM51422  
ID AAM51422 standard; peptide; 6 AA.

XX  
AC AAM51422;  
XX  
DT 08-JAN-2002 (first entry)  
XX  
DE Integrin activating peptide SEQ ID NO 1.  
XX  
XX Integrin stimulant; vulnerary; injury healing;  
KW postsurgical tissue recovery.  
XX  
XX Unidentified.

OS  
XX JP2001213898-A.  
XX  
XX 07-AUG-2001.  
PD  
XX 31-JAN-2000; 2000JP-0022469.  
PF  
XX 31-JAN-2000; 2000JP-0022469.  
PR  
XX (HISM ) HISAKITSU PHARM CO LTD.  
PA  
XX WPI; 2001-629610/73.  
DR  
XX

XX An injury healing and postsurgical tissue recovering integrin  
PT activating peptide -  
XX  
XX Claim 1; Page 3; 11pp; Japanese.

XX The invention relates to novel peptides with vulnerary activity, useful  
CC for injury healing and postsurgical tissue recovery by acting as an  
CC integrin stimulant.  
CC  
XX

SQ Sequence 6 AA;  
  
Query Match 54.3%; Score 19; DB 22; Length 6;  
Best Local Similarity 60.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FTTLT 7  
: |||  
Db 1 YTITI 5

RESULT 15  
AAB97355  
ID AAB97355 standard; peptide; 6 AA.

XX  
AC AAB97355;  
XX  
DT 15-AUG-2001 (first entry)  
XX  
DE A05 epitope used in dual labelled receptor construction.  
XX  
KW Automated measurement; cell viability; epitope tag; luminescence;  
KW G-protein coupled receptor; high content screen.  
XX  
OS Synthetic.  
XX  
PN WO200135072-A2.

XX  
XX 17-MAY-2001.  
PF 09-NOV-2000; 2000WO-US30896.  
XX  
PR 09-NOV-1999; 99US-0164353.  
PR 19-JAN-2000; 2000US-0176504.

XX  
PA (CELL-) CELLOMICS INC.  
XX  
PI Gosh RN, Debiasio R, Chen Y, Bellutta P, Giuliano K, Pasley JW;  
XX WPI; 2001-329169/34.

XX Automated measurement of cell viability, involves contacting cells with  
PT luminescent reporter molecule, imaging cells to get signals, converting  
PT signals into digital data and using data to measure viable cell -  
XX  
PS Example 6; Page 52; 155pp; English.

XX This invention relates to a method for the automated measurement of cell  
CC viability. The method involves contacting cells with luminescent  
CC reporter molecules, imaging cells to get signals, and converting the  
CC signals into digital data which can be used as a measurement of cell  
CC viability. Included in the invention is a computer readable storage  
CC medium comprising a programme which causes the method of the invention  
CC to be activated. The method is useful for cell state identification in  
CC cells. The method is also useful for drug discovery. An example of the  
CC invention relates to the use of inserted sequences and their ligands for  
CC high content screens incorporating dual labelled receptors. The present  
CC sequence represents an epitope tag used to label one end of a G-protein  
CC coupled receptor (GPCR). The intracellular and extracellular domains of  
CC the GPCR are distinctly labelled so that using the method of the  
CC invention the extent of internalisation of the receptor can be measured.

XX  
SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 22; Length 6;  
Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
: |||  
Db 1 TDFYL 5

Search completed: October 4, 2003, 12:45:23  
Job time : 52.6667 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: October 4, 2003, 12:46:43 ; Search time 33.6657 Seconds  
(without alignments)  
32.896 Million cell updates/sec

Title: US-09-712-819C-5

Perfect score: 35

Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCRUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	54.3	5	12	US-10-315-964A-394 Sequence 394, App
2	19	54.3	5	12	US-10-317-251A-394 Sequence 394, App
3	19	54.3	5	12	US-10-317-252A-394 Sequence 394, App
4	19	54.3	6	12	US-10-315-964A-402 Sequence 402, App
5	19	54.3	6	12	US-10-317-251A-402 Sequence 402, App
6	19	54.3	6	12	US-10-317-252A-402 Sequence 402, App
7	19	54.3	6	15	US-10-083-815-4 Sequence 4, App
8	18	51.4	6	14	US-10-156-820-59 Sequence 59, App
9	17	48.6	5	11	US-09-788-006-107 Sequence 107, App
10	17	48.6	5	11	US-09-788-006-108 Sequence 108, App
11	17	48.6	5	12	US-10-348-504-132 Sequence 132, App
12	17	48.6	5	12	US-10-407-123-76 Sequence 76, Appl
13	17	48.6	6	10	US-09-770-102A-55 Sequence 55, Appl
14	17	48.6	6	12	US-10-172-919-25 Sequence 25, Appl
15	17	48.6	7	11	US-09-954-385-257 Sequence 257, App

16	45.7	6	12	US-10-286-993-5	Sequence 5, Appl
17	45.7	7	9	US-09-832-723-69	Sequence 69, Appl
18	45.7	7	12	US-10-303-331-69	Sequence 69, Appl
19	45.7	7	14	US-10-060-100-93	Sequence 93, Appl
20	42.9	5	11	US-09-788-006-2	Sequence 2, Appl
21	42.9	5	12	US-09-788-006-3	Sequence 3, Appl
22	42.9	5	12	US-10-286-186-3	Sequence 3, Appl
23	42.9	5	12	US-10-286-186-4	Sequence 4, Appl
24	42.9	5	15	US-10-214-796-21	Sequence 21, Appl
25	42.9	6	10	US-09-293-854-3	Sequence 8, Appl
26	42.9	6	11	US-09-990-586-8	Sequence 8, Appl
27	42.9	6	12	US-10-310-113-2	Sequence 8, Appl
28	42.9	6	15	US-10-105-930-39	Sequence 39, Appl
29	42.9	6	15	US-10-006-869-650	Sequence 650, App
30	42.9	6	15	US-10-293-417-8	Sequence 8, Appl
31	42.9	7	9	US-09-734-417-12	Sequence 12, Appl
32	42.9	7	11	US-09-884-456-27	Sequence 27, Appl
33	42.9	7	11	US-09-281-495-19	Sequence 19, Appl
34	42.9	7	12	US-10-052-578-172	Sequence 172, App
35	42.9	7	12	US-10-271-708-14	Sequence 14, Appl
36	42.9	7	12	US-10-053-520-172	Sequence 172, App
37	42.9	7	14	US-10-050-552A-4	Sequence 4, Appl
38	42.9	7	15	US-10-006-869-651	Sequence 651, App
39	42.9	7	15	US-10-006-869-653	Sequence 653, App
40	42.9	7	15	US-10-044-692-142	Sequence 142, App
41	42.9	7	15	US-10-044-539-142	Sequence 142, App
42	40.0	5	9	US-09-804-866-11	Sequence 11, Appl
43	40.0	5	11	US-09-890-748-2203	Sequence 2203, Ap
44	40.0	5	15	US-10-214-796-18	Sequence 18, Appl
45	40.0	6	10	US-09-727-963A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-10-315-964A-394  
; Sequence 394, Application US/10315964A  
; Publication No. US20030148956A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert C  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M3  
; CURRENT APPLICATION NUMBER: US/10/315,964A  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 394  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-315-964A-394

Query Match 54.3%; Score 19; DB 12; Length 5;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy : TDFTL 5

Db 1 TKFTL 5

RESULT 2  
US-10-317-251A-394  
; Sequence 394, Application US/10317251A  
; Publication No. US20030148957A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M2  
; CURRENT APPLICATION NUMBER: US/10/317,251A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/383,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 394  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-251A-394

Query Match 54.3%; Score 19; DB 12; Length 5;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
| | | |  
Db 1 TKFTL 5  
RESULT 3  
US-10-317-252A-394  
; Sequence 394, Application US/10317252A  
; Publication No. US20030148958A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M  
; CURRENT APPLICATION NUMBER: US/10/317,252A  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/383,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 394  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-252A-394

Query Match 54.3%; Score 19; DB 12; Length 5;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
| | | |  
Db 1 TKFTL 5  
RESULT 4  
US-10-315-964A-402  
; Sequence 402, Application US/10315964A  
; Publication No. US20030148956A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M3  
; CURRENT APPLICATION NUMBER: US/10/315,964A  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 402  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-315-964A-402

Query Match 54.3%; Score 19; DB 12; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
| | | |  
Db 2 TKFTL 6  
RESULT 5  
US-10-317-251A-402  
; Sequence 402, Application US/10317251A  
; Publication No. US20030148957A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M2  
; CURRENT APPLICATION NUMBER: US/10/317,251A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 402  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-251A-402

US-10-317-251A-402

Query Match 54.3%; Score 19; DB 12; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
Db 2 TKFTL 6

RESULT 6

US-10-317-252A-402  
; Sequence 402, Application US/10317252A  
; Publication No. US20030148958A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M  
; CURRENT APPLICATION NUMBER: US/10/317,252A  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 402  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-252A-402

Query Match 54.3%; Score 19; DB 12; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
Db 2 TKFTL 6

RESULT 7

US-10-083-815-4  
; Sequence 4, Application US/10083815  
; Publication No. US20030026781A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Clevenger, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING  
; TITLE OF INVENTION: ENDOGENOUS INHIBITOR OF ATP SYNTHASE, INCLUDING  
; TITLE OF INVENTION: TREATMENT FOR DIABETES  
; FILE REFERENCE: 66088.435C2  
; CURRENT APPLICATION NUMBER: US/10/083,815  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Epitope tag  
US-10-083-815-4

Query Match 54.3%; Score 19; DB 12; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5  
Db 2 TDFYL 5

RESULT 8

US-10-156-820-59  
; Sequence 59, Application US/10156820  
; Publication No. US20020150558A1  
; GENERAL INFORMATION:  
; APPLICANT: Boulianger, Pierre  
; APPLICANT: Hong, Saw See  
; APPLICANT: Karayan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
; FILE REFERENCE: 032751-036  
; CURRENT APPLICATION NUMBER: US/10/156,820  
; CURRENT FILING DATE: 2002-06-30  
; PRIOR APPLICATION NUMBER: PCT/FR98/00184  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: FR 97/01005  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: FR 97/11166  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Phagotome  
US-10-156-820-59

Query Match 51.4%; Score 18; DB 14; Length 6;  
Best Local Similarity 60.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLT 6  
Db 2 NYTLT 6

RESULT 9

US-09-788-006-107  
; Sequence 107, Application US/09788006  
; Publication No. US20030036093A1  
; GENERAL INFORMATION:  
; APPLICANT: Floudas, Christopher A.  
; APPLICANT: Klepeis, John L.  
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets,  
; TITLE OF INVENTION: Polypeptide Tertiary Structures  
; FILE REFERENCE: PC-0007  
; CURRENT APPLICATION NUMBER: US/09/788,006  
; CURRENT FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 107  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Streptomyces griseus  
US-09-788-006-107

Query Match 48.6%; Score 17; DB 11; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FTLT 6  
Db 2 FTVT 5



SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-10-407-123-76

Query Match 48.6%; Score 17; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4  
|||  
Db 1 DFT 3

RESULT 13

US-09-770-102A-55  
Sequence 55, Application US/09770102A  
Publication No. US20020197506A1  
GENERAL INFORMATION:  
APPLICANT: Cyclacel  
TITLE OF INVENTION: Compositions and Methods for Monitoring the Modification of Modified Polypeptides  
FILE REFERENCE: 10069/1062  
CURRENT APPLICATION NUMBER: US/09/770,102A  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 60/179283  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 55  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Tag peptide  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(6)  
OTHER INFORMATION: Tag peptide  
US-09-770-102A-55

Query Match 48.6%; Score 17; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TDF 3  
|||  
Db 1 TDF 3

RESULT 14

US-10-172-919-25  
Sequence 25, Application US/10172919  
Publication No. US20010152947A1  
GENERAL INFORMATION:  
APPLICANT: CRCSSMAN, DAVID C.  
APPLICANT: DUFF, GORDON W.  
APPLICANT: FRANCIS, SHEILA E.  
APPLICANT: KORNMAN, KENNETH S.  
APPLICANT: BARNETT, KATHERINE  
TITLE OF INVENTION: METHODS FOR DETECTING AND TREATING THE EARLY ONSET OF AGING-RELATED CONDITIONS  
FILE REFERENCE: MSA-025.01  
CURRENT APPLICATION NUMBER: US/10/172,919  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: 60/298,493  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: illustrative  
OTHER INFORMATION: peptide

US-10-172-919-25

Query Match 48.6%; Score 17; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TDF 3  
|||  
Db 2 TDF 4

RESULT 15

US-09-954-385-257  
Sequence 257, Application US/09954385  
Publication No. US20030100467A1  
GENERAL INFORMATION:  
APPLICANT: Ahle, Wolfgang  
APPLICANT: Baldwin, Toby L.  
APPLICANT: Van Gastel, Franciscus J.C.  
APPLICANT: Janssen, Gisele G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huaming  
APPLICANT: Winetzky, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
FILE REFERENCE: GC690  
CURRENT APPLICATION NUMBER: US/09/954,385  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 433  
SOFTWARE: FastSEQ for Windows Version. 4.0  
SEQ ID NO 257  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding peptide  
US-09-954-385-257

Query Match 48.6%; Score 17; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
Db 1 TDF 3

Search completed: October 4, 2003, 13:05:04  
Job time : 34.6667 secs

GenCore version 5.1.1.6  
Copyright: (c) 1993-2003 CompuGen Ltd.

TM protein - protein search, using sw model

Run on: October 4, 2003, 12:42:47 ; Search time 17 seconds  
(without alignments)  
17,422 Million cell updates/sec

Title: US-09-712-819C-5  
Perfect score: 35  
Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231358 residues

Total number of hits satisfying chosen parameters: 49738

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTJS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	54.3	6	4	US-09-140-084-4
2	19	54.3	6	4	US-09-724-297-4
3	19	54.3	7	3	US-08-916-443A-8
4	19	54.3	7	3	US-08-640-737-38
5	18	51.4	6	4	US-09-155-613A-59
6	17	48.6	5	1	US-08-405-230-10
7	17	48.6	5	2	US-08-910-990-10
8	17	48.6	5	4	US-09-367-777-132
9	17	48.6	5	4	US-09-367-791A-76
10	17	48.6	6	4	US-09-233-857-7
11	17	48.6	7	1	US-08-136-743B-29
12	17	48.6	7	1	US-08-136-743B-30
13	17	48.6	7	1	US-08-136-743B-31
14	17	48.6	7	1	US-08-136-743B-32
15	17	48.6	7	1	US-08-405-230-5
16	17	48.6	7	2	US-08-910-990-5
17	17	48.6	7	2	US-08-739-401A-6
18	17	48.6	7	5	PCT-US93-11703-72
19	16	45.7	5	1	US-08-180-203B-14
20	16	45.7	5	1	US-08-385-745-14
21	16	45.7	5	3	US-08-591-632-17
22	16	45.7	5	3	US-08-591-632-23
23	16	45.7	5	3	US-08-591-632-26
24	16	45.7	5	3	US-08-485-368-14
25	16	45.7	5	3	US-08-474-853-14
26	16	45.7	5	4	US-09-166-205B-14
27	16	45.7	5	4	US-09-611-451-17

28	16	45.7	5	4	US-09-611-451-23	Sequence 23, Appl
29	16	45.7	5	4	US-09-611-451-26	Sequence 26, Appl
30	16	45.7	5	5	PCT-US94-02629-14	Sequence 14, Appl
31	16	45.7	6	1	US-08-252-995D-7	Sequence 7, Appl
32	16	45.7	6	2	US-08-482-228-190	Sequence 180, App
33	16	45.7	6	2	US-08-834-108-7	Sequence 7, Appl
34	16	45.7	6	3	US-08-482-528-180	Sequence 180, App
35	16	45.7	7	1	US-08-136-743B-55	Sequence 55, Appl
36	16	45.7	7	1	US-08-096-946-5	Sequence 5, Appl
37	16	45.7	7	2	US-08-177-109A-7	Sequence 7, Appl
38	16	45.7	7	2	US-08-697-706-7	Sequence 7, Appl
39	16	45.7	7	3	US-09-640-216-28	Sequence 28, Appl
40	16	45.7	7	3	US-09-173-941-52	Sequence 52, Appl
41	16	45.7	7	5	PCT-US94-07329-5	Sequence 5, Appl
42	15	42.9	5	1	US-08-136-743B-63	Sequence 63, Appl
43	15	42.9	5	1	US-07-789-184-126	Sequence 126, App
44	15	42.9	5	1	US-08-475-263-126	Sequence 126, App
45	15	42.9	5	1	US-08-485-886-126	Sequence 126, App

ALIGNMENTS

RESULT 1  
US-09-140-084-4  
; Sequence 4, Application US/09140084A  
; Patent No. 6300065  
; GENERAL INFORMATION:  
; APPLICANT: Kieck, et al.  
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof  
; FILE REFERENCE: D6061CIP2  
; CURRENT APPLICATION NUMBER: US/09/140,084A  
; CURRENT FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Epitope Tag  
US-09-140-084-4

Query Match: 54.3%; Score 19; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TDFTL 5  
|||  
Db 1 TDFYL 5

RESULT 2  
US-09-724-297-4  
; Sequence 4, Application US/09724297  
; Patent No. 6423538  
; GENERAL INFORMATION:  
; APPLICANT: The Board of Trustees of the University of Illinois  
; APPLICANT: Wittrup, et al.  
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof  
; FILE REFERENCE: 97-99C  
; CURRENT APPLICATION NUMBER: US/09/724,297  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/009,388  
; PRIOR FILING DATE: 1998-01-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: unknown  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION: {}...()  
OTHER INFORMATION: Epitope tag  
US-09-724-297-4

Query Match 54.3%; Score 19; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFTLT 5  
Db 1 DFTLT 5

## RESULT 3

US-08-916-443A-8  
Sequence 8, Application US/08916443A  
Patent No. 6001986

## GENERAL INFORMATION:

APPLICANT: Yong Sig KIM  
APPLICANT: Sun Chung PARK  
APPLICANT: Seo Kyung OH  
APPLICANT: Hosuli LEE  
APPLICANT: Geong Woo CHO  
APPLICANT: Chang H. CHUNG  
TITLE OF INVENTION: Antiviral Proteins, Awarandin 1 and 2, from  
TITLE OF INVENTION: Amananthus Viridis, DNAs Encoding Therefrom  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3+ Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: WordPerfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/916,443A  
FILING DATE: 22 AUG 1997  
CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 33,046  
REFERENCE/DOCKET NUMBER: 1942/18  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776  
TELEFAX: 202-429-0796

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-916-443A-8

Query Match 54.3%; Score 19; DB 3; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DFTLT 7  
Db 2 DLTFTV 7

## RESULT 4

US-08-640-737-38  
Sequence 38, Application US/08640737  
Patent No. 6215044

## GENERAL INFORMATION:

Query Match 51.4%; Score 18; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;



Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFLT 6  
Db 2 NYTUT 6

RESULT 6

US-08-405-230-10  
; Sequence 10, Application US/08405230  
; Patent No. 5707846  
; GENERAL INFORMATION:  
; APPLICANT: TANIGUCHI, Naoyuki  
; APPLICANT: NISHIKAWA, Atsushi  
; APPLICANT: YAMAGUCHI, No. 5707846om1  
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE  
; TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: George Mason Bldg., Washington & Prince Sts.  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/405,230  
; FILING DATE: 16-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/110,736  
; FILING DATE: 23-AUG-1993  
; APPLICATION NUMBER: JP 4-245950  
; FILING DATE: 24-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-237118  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E  
; REGISTRATION NUMBER: 36,113  
; REFERENCE/DOCKET NUMBER: 001560-215  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..5  
; OTHER INFORMATION: /note="Amino acid sequence  
; OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO. 7."

US-08-405-230-10

Query Match 48.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
Db 2 TDF 4

RESULT 7

US-08-910-990-10  
; Sequence 10, Application US/08910990  
; Patent No. 5834284  
; GENERAL INFORMATION:  
; APPLICANT: TANIGUCHI, Naoyuki  
; APPLICANT: NISHIKAWA, Atsushi  
; APPLICANT: YAMAGUCHI, No. 5834284om1  
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE  
; TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: George Mason Bldg., Washington & Prince Sts.  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,990  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/405,230  
; FILING DATE: 16-MAR-1995  
; APPLICATION NUMBER: US 08/110,736  
; FILING DATE: 23-AUG-1993  
; APPLICATION NUMBER: JP 4-245950  
; FILING DATE: 24-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-237118  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E  
; REGISTRATION NUMBER: 36,113  
; REFERENCE/DOCKET NUMBER: 001560-215  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..5  
; OTHER INFORMATION: /note="Amino acid sequence  
; OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO. 7."

US-08-910-990-10

Query Match 48.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
Db 2 TDF 4

RESULT 8

US-09-367-777-132  
; Sequence 132, Application US/09367777  
; Patent No. 6562598  
; GENERAL INFORMATION:  
; APPLICANT: Himmelspach, Michele  
; Pflaederer, Michael

Falkner, Falko-Guenther  
Eibl, Johann  
Dorner, Friedrich  
Schlokot, Uwe  
TITLE OF INVENTION: Factor X Deletion Mutants  
and Analogues Thereof  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/367,777  
FILING DATE: 10-NO. 6562598-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AT A 336/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT93/00016  
FILING DATE: 27-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 20695D-000920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-09-367-777-132

Query Match 48.6%; Score 17; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4  
|||  
Db 1 DFT 3

RESULT 9  
US-09-367-791A-76  
; Sequence 76, Application US/09367791A  
; Patent No. 6573071  
; GENERAL INFORMATION:  
; APPLICANT: Hammelspach, Michele  
; Schlokot, Uwe  
; Dorner, Friedrich  
; Fisch, Andreas  
; Eibl, Johann  
; TITLE OF INVENTION: Factor X Analogues With  
; a Modified Protease Cleavage Site  
NUMBER OF SEQUENCES: 122  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/367,791A  
FILING DATE: 12-NO. 6573071-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AT A 335/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00045  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,471  
REFERENCE/DOCKET NUMBER: 20695D-000720US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-367-791A-76

Query Match 48.6%; Score 17; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4  
|||  
Db 1 DFT 3

RESULT 10  
US-09-233-857-7  
; Sequence 7, Application US/09233857  
; Patent No. 6495353  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory  
; APPLICANT: Flanagan, Peter  
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART  
; FILE REFERENCE: 239/251  
; CURRENT APPLICATION NUMBER: US/09/233,857  
; CURRENT FILING DATE: 1999-01-20  
; EARLIER APPLICATION NUMBER: USSN 60/372,023  
; EARLIER FILING DATE: 1998-01-21  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-233-857-7

Query Match 48.6%; Score 17; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
Db 3 TDF 5

## RESULT 11

US-08-136-743B-29  
Sequence 29, Application US/08136743B  
Patent No. 5459063  
GENERAL INFORMATION:  
APPLICANT: Barry S. Cooperman, Harvey Rubin,  
APPLICANT: Jerome Salem, and Allison L. Fisher  
TITLE OF INVENTION: "Plasmodium falciparum Ribonu-  
TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-  
TITLE OF INVENTION: Thereof"  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The University of Pennsylvania  
STREET: Suite 330  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19104-3246

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/136,743B

FILING DATE: 10/14/93

CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 3957-10

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5459063e

INFORMATION FOR SEQ ID NO: 29:

## SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-136-743B-29

Query Match 48.6%; Score 17; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
Db 5 TDF 7

## RESULT 12

US-08-136-743B-30  
Sequence 30, Application US/08136743B  
Patent No. 5459063  
GENERAL INFORMATION:  
APPLICANT: Barry S. Cooperman, Harvey Rubin,  
APPLICANT: Jerome Salem, and Allison L. Fisher  
TITLE OF INVENTION: "Plasmodium falciparum Ribonu-  
TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-  
TITLE OF INVENTION: Thereof"  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The University of Pennsylvania  
STREET: Suite 330  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19104-3246

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/136,743B  
FILING DATE: 10/14/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 3957-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5459063e  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-136-743B-30

Query Match 48.6%; Score 17; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
Db 5 TDF 7

## RESULT 13

US-08-136-743B-31

Sequence 31, Application US/08136743B

Patent No. 5459063

## GENERAL INFORMATION:

APPLICANT: Barry S. Cooperman, Harvey Rubin,

APPLICANT: Jerome Salem, and Allison L. Fisher

TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-

TITLE OF INVENTION: Thereof"

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: The University of Pennsylvania

STREET: Suite 330

STREET: 3700 Market Street

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19104-3246

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/136,743B

FILING DATE: 10/14/93

CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 3957-10

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5459063e

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-136-743B-31

Query Match 48.6%; Score 17; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
DB 5 TDF 7

## RESULT 14

US-08-136-743B-32

; Sequence 32, Application US/08136743B

; Patent No. 5459063

; GENERAL INFORMATION:

; APPLICANT: Barry S. Cooperman, Harvey Rubin,

; APPLICANT: Jerome Salem, and Alison L. Fisher

; TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-

; TITLE OF INVENTION: thereof"

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The University of Pennsylvania

; STREET: Suite 330

; STREET: 3700 Market Street

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19104-3246

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DCS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/136.743B

; FILING DATE: 10/14/93

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 3957-10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX: No. 5459063e

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-09-136-743B-32

Query Match 48.6%; Score 17; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
DB 5 TDF 7

## RESULT 15

US-08-405-230-5

; Sequence 5, Application US/08405230

; Patent No. 5707846

; GENERAL INFORMATION:

; APPLICANT: TANIGUCHI, Naoyuki

; APPLICANT: NISHIKAWA, Atsushi

; APPLICANT: YAMAGUCHI, No. 5707846cm1

; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE

; TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF

; NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker &amp; Mathis

; STREET: George Mason Bldg., Washington &amp; Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/405.230

; FILING DATE: 16-MAR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/110,736

; FILING DATE: 23-AUG-1993

; APPLICATION NUMBER: JP 4-24595C

; FILING DATE: 24-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-237118

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Crane-Feury, Sharon E

; REGISTRATION NUMBER: 36,113

; REFERENCE/DOCKET NUMBER: CO:560-215

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-405-230-5

Query Match 48.6%; Score 17; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3  
|||  
DB 2 TDF 4

Search completed: October 4, 2003, 12:50:34  
Job time : 18 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:52 ; Search time 19.3333 Seconds  
(without alignments)  
34.820 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1: FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168652 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	45.5	7	2	S19630 ribosomal protein
2	13	39.4	7	2	A28709 phosphonoacetaldeh
3	12	36.4	5	2	T14910 hypothetical prote
4	11	33.3	5	2	P10644 T-cell receptor be
5	10	30.3	7	2	PS0254 18K protein 5507 -
6	9	27.3	3	3	T13892 cytochrome-c oxida
7	9	27.3	4	2	I40604 endoglucanase F -
8	9	27.3	4	2	T46627 hypothetical prote
9	9	27.3	5	2	A60521 glycogen phosphory
10	9	27.3	5	2	E42364 flagellar protein
11	9	27.3	5	2	A44955 alkalal monooxygen
12	9	27.3	5	2	S11127 phosphoprotein, bo
13	9	27.3	5	2	PT0525 T-cell receptor be
14	9	27.3	5	2	PT0577 T-cell receptor be
15	9	27.3	5	2	PT0565 T-cell receptor be
16	9	27.3	5	2	PT0700 T-cell receptor be
17	9	27.3	5	2	S69237 surface protein te
18	9	27.3	6	2	A60986 N-formyl oligopept
19	9	27.3	6	2	A43766 28K ubiquitin-immu
20	9	27.3	6	2	I37263 Y protein - human
21	9	27.3	6	2	B26206 alpha-1,4-glucan-p
22	9	27.3	6	2	I65846 MHC H2-L antigen -
23	9	27.3	6	2	PT0518 T-cell receptor be
24	9	27.3	6	2	PT0662 T-cell receptor be
25	9	27.3	6	2	I49424 cytotoxic T-lympho
26	9	27.3	7	2	CN0859 peptidyl-dipeptida
27	9	27.3	7	2	A15398 choline oxidase 12
28	9	27.3	7	2	B39127 phosphotransferase
29	9	27.3	7	2	S25266 pilE protein - Esc

30	9	27.3	7	2	A25269 sex pheromone CAM3
31	9	27.3	7	2	A30812 sex pheromone CCF1
32	9	27.3	7	2	PN0150 omega-glucadine 1,
33	9	27.3	7	2	S78024 ribosomal protein
34	9	27.3	7	2	E48394 glycoprotein compo
35	9	27.3	7	2	I48086 DNA topoisomerase
36	9	27.3	7	2	PT0671 T-cell receptor be
37	9	27.3	7	2	S66442 glutathione S-tran
38	9	27.3	7	2	B48394 major fat-globule
39	9	27.3	7	2	PN0649 polyluanase (EC 3.
40	9	27.3	7	2	S09056 globulin IV alpha
41	8	24.2	4	2	I40505 hypothetical prote
42	8	24.2	5	2	I39964 ribosomal protein
43	8	24.2	5	2	I39966 ribosomal protein
44	8	24.2	5	2	I39965 ribosomal protein
45	8	24.2	5	2	B22565 R-phycocerythrin al

ALIGNMENTS

RESULT 1

S19630

ribosomal protein L30 - Streptomyces griseus (fragment)

C:Species: Streptomyces griseus

C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 06-Jun-1997

C:Accession: S19630

R:Ochi, K.

Int. J. Syst. Bacteriol. 42, 144-150, 1992

A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete

A:Reference number: S19630; MUID:92144363; PMID:1736962

A:Accession: S19630

A:Molecule type: protein

A:Residues: 1-7 <OCH>

A:Experimental source: strain IFO 13189

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match 45.5%; Score 15; DB 2; Length 7;

Best Local Similarity 60.0%; Pred. No. 2.9e-05;

Matches 3; Conservative 2; Mismatches 0; Indels 3; Gaps 0;

QY 3 LKISR 7

Db 3 LKITQ 7

RESULT 2

A28709

phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)

C:Species: Bacillus cereus.

C>Date: 22-Aug-1988 #sequence\_revision 22-Aug-1988 #text\_change 30-Sep-1993

C:Accession: A28709

R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.

Biochemistry 27, 2229-2234, 1988

A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidenc

A:Reference number: A28709; MUID:88241058; PMID:3132206

A:Accession: A28709

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <OLS>

Query Match

Best Local Similarity 39.4%; Score 13; DB 2; Length 7;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKI 5

Db 1 LKI 3

RESULT 3

T14910  
hypothetical protein - parsley  
C:Species: Petroselinum crispum (parsley)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: T14910  
R:Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Prohmeyer, H.  
Mol.Gen. Genet. 257, 595-605, 1998  
A:Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of  
A:Reference number: Z18261; MUID:98265918; PMID:9604882  
A:Accession: T14910  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5 <KIR>  
A:Cross-references: EMBL:Y10810; NID:G3336904; PID:CAA71769.1; PID:G3336905  
A:Experimental source: ssp. Hamburger Schnitt

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7  
|||  
DB 2 VSR 4

RESULT 4  
PT0644  
T-cell receptor beta chain V-D-J region (111-16) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0644  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PTC509; MUID:91277601; PMID:1711558  
A:Accession: PT0644  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FEE>  
A:Experimental source: newborn thymus, strain RAJE/c  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
|||  
DB 4 FT 5

RESULT 5  
PS0254  
18K protein 5507 - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
C:Accession: PS0254  
R:Tsugita, A.  
Submitted to JIPID, April 1993  
A:Reference number: PS0206  
A:Accession: PS0254  
A:Molecule type: protein  
A:Residues: 1-7 <TSU>  
A:Experimental source: leaf, chloroplast, strain Nihonbare  
A>Note: molecular weight 18K, pI 4.4

Query Match 30.3%; Score 10; DB 2; Length 7;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKISR 7  
| : :  
DB 1 LAIAK 5

RESULT 6  
T13892  
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f  
C:Species: Mitochondrion Lampetra fluviatilis (river lamprey)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: T13892  
R:Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the  
A:Reference number: Z17775; MUID:97398704; PMID:9254918  
A:Accession: T13892  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3 <DEL>  
A:Cross-references: EMBL:Y09528; NID:G2340016; PID:CAA70721.1; PID:G4379123  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
|||  
DB 2 TL 3

RESULT 7  
I40804  
endoglucanase F - Clostridium thermocellum (fragment)  
C:Species: Clostridium thermocellum  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Aug-1996  
C:Accession: I40804  
R:Mishra, S.; Beguin, P.; Aubert, J.  
J. Bacteriol. 173, 80-85, 1991  
A:Title: Transcription of clostridium thermocellum endoglucanase genes celf and celd  
A:Reference number: I40804; MUID:91100322; PMID:1987137  
A:Accession: I40804  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <RES>  
A:Cross-references: GB:M64363; NID:G144771  
C:Genetics:  
A:Gene: celf  
A:Start codon: TTG

Query Match 27.3%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5  
|||  
DB 3 KI 4

RESULT 8  
T46627  
hypothetical protein c4 - loblolly pine  
C:Species: Pinus taeda (loblolly pine)  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
C:Accession: T46627  
R:Chang, S.; Puryear, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.  
Submitted to the EMBL Data Library, July 1995  
A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is  
A:Reference number: Z23105  
A:Accession: T46627  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <CHA>

A;Cross-references: EMBL:U31109; NID:G974285; PID:G974293  
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 27.3%; Score 9; DB 2; Length 4;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK1 5  
Db 1 MKL 3

RESULT 9  
A60521  
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N;Alternate names: glycogen phosphorylase b  
C;Species: Liza ramada  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
C;Accession: A60521  
R;Bonamusa, L.; Baanante, I.V.  
Comp. Biochem. Physiol. B 95, 295-301, 1990  
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle  
A;Reference number: A60521; MUID:90222907; PMID:2109663  
A;Accession: A60521  
A;Molecule type: protein  
A;Residues: 1-5 <BON>  
C;Superfamily: phosphorylase  
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimental

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIS 6  
Db 1 QIS 3

RESULT 10  
E42364  
flagellar protein flhR - Salmonella typhimurium (fragment)  
C;Species: Salmonella typhimurium  
C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
C;Accession: E42364  
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991  
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
A;Reference number: A42364; MUID:91258342; PMID:164620;  
A;Accession: E42364  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <VOG>  
A;Cross-references: GB:M62408

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3  
Db 3 TL 4

RESULT 11  
A44955  
alkanal monooxygenase (FMN-linked) (EC 1.1.4.14.3) alpha chain - Vibrio harveyi (fragment)  
C;Species: Vibrio harveyi  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C;Accession: A44955  
R;Paquette, O.; Tu, S.C.  
Photochem. Photobiol. 50, 817-825, 1989  
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib

A;Reference number: A44955; MUID:90175700; PMID:2626493  
A;Accession: A44955  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <PAQ>  
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7  
Db 3 IXR 5

RESULT 12  
S11127  
phosphoprotein, bone - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Mar-2000  
C;Accession: S11127; S11128  
R;Mikuni-Takagaki, Y.; Glimcher, M.J.  
Biochem. J. 268, 585-591, 1990  
A;Title: Post-translational processing of chicken bone phosphoproteins. Identification  
A;Reference number: S11127; MUID:90303246; PMID:2363696  
A;Accession: S11127  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <MIK1>  
A;Accession: S11128  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 'X', 2-5 <MIK2>  
C;Keywords: phosphoprotein

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7  
Db 3 VSK 5

RESULT 13  
PT0525  
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0525  
R;Feeney, A.J.  
C. Exp. Med. 174, 115-124, 1991  
A;Title: Functional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0525  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: adult thymus, strain BA1B/c  
C;Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7  
Db 2 SR 3

RESULT 14  
PT0577

T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0577; PT0574  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0569; MUID:91277601; PMID:1711558  
A:Accession: PT0577  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC  
A:Accession: PT0574  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1C  
C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7  
|  
Db 3 SR 4

## RESULT 15

PT0565  
T-cell receptor beta chain V-D-J region (141-1CF) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0565  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0569; MUID:91277601; PMID:1711558  
A:Accession: PT0565  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7  
|  
Db 3 SR 4

Search completed: October 4, 2003, 12:49:38  
Job time : 20.3333 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw mode!

Run on: October 4, 2003, 12:27:32 ; Search time 10 Seconds  
(without alignments)  
32.919 Million cells updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FPKISR ?

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 83

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	33.3	5	1 RE31_LITRU	P82072 Litoria rub
2	11	33.3	5	1 RE32_LITRU	P82073 Litoria rub
3	10	30.3	7	1 GERP_MOUSE	P99025 mus musculu
4	9	27.3	5	1 UF01_MOUSE	P38639 mus musculu
5	9	27.3	6	1 UN06_CLOPA	P81351 Clostridium
6	9	27.3	7	1 CCF1_ENTPA	P20104 enterococcu
7	9	27.3	7	1 CHOX_ALCSP	P16101 alcaligenes
8	9	27.3	7	1 CIA_ENTPA	P11932 enterococcu
9	9	27.3	7	1 UC24_MAIZE	P80630 zea mays (m
10	8	24.2	5	1 AL14_CARMA	P81817 carcinus ma
11	8	24.2	5	1 PSK_DAUCA	P58261 daucus caro
12	8	24.2	7	1 ALL2_CARMA	P81905 carcinus ma
13	8	24.2	7	1 ALL3_CARMA	P81806 carcinus ma
14	8	24.2	7	1 ALL4_CARMA	P81807 carcinus ma
15	8	24.2	7	1 ALL5_CARMA	P81808 carcinus ma
16	8	24.2	7	1 ALL7_CYPPO	P82158 cydia pomon
17	8	24.2	7	1 CARP_MYTEC	P10420 mytilus edu
18	8	24.2	7	1 FARS_HIRME	P42564 hiruado medi
19	7	21.2	3	1 LUXE_VIBFI	P24272 vibrio fisc
20	7	21.2	6	1 LOK1_LOCM1	P41491 locusta mig
21	7	21.2	6	1 VP19_HSVIK	P23210 herpes simp
22	6	18.2	4	1 ACH1_ACHFU	P35904 achatina fu
23	6	18.2	4	1 FAR3_HIRME	P42562 hiruado medi
24	6	18.2	4	1 FAR4_HIRME	P42563 hiruado medi
25	6	18.2	4	1 FFKA_ATEIL	P58705 anthopleura
26	6	18.2	4	1 FLRF_HIRME	P42561 hiruado medi
27	6	18.2	4	1 FLRN_ATEIL	P58707 anthopleura
28	6	18.2	4	1 FMRF_MAGNI	P01162 macrocallis
29	6	18.2	4	1 FYRI_ATEIL	P58706 anthopleura
30	6	18.2	4	1 OCPI_CCTNI	P58648 octopus min
31	6	18.2	5	1 EI03_LITRU	P82099 Litoria rub
32	6	18.2	5	1 EI04_LITRU	P82100 Litoria rub
33	6	18.2	5	1 FARP_ARTTR	P41853 artiopesthi

RESULT 1  
RE31\_LITRU  
ID RE31\_LITRU STANDARD; PRT: 5 AA.  
AC P82072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie C.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT 'The structure of new peptides from the Australian red tree frog  
'Litoria rubella'. The skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.';  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: Shows neither neuroptide activity nor antibiotic  
activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.  
KW Amphibian defense peptide; Amidation.  
FT MCD RES 5 5  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB1C30000C CRC64;  
Query Match 33.3%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
DB 4 FT 5

RESULT 2  
RE32\_LITRU  
ID RE32\_LITRU STANDARD; PRT: 5 AA.  
AC P82073;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A2A33000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 ||  
 Db 4 FT 5

## RESULT 3

GFRP\_MOUSE  
 ID GFRP\_MOUSE STANDARD; PRT; 7 AA.  
 AC P99025;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).  
 DE GCHFR OR GFRP.  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
 RA Cowthorne M.;  
 RJ Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MEDIATES TETRAHYDROBIPTERIN INHIBITION OF GTP  
 CC CYCLOHYDROLASE 1. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE  
 CC (BY SIMILARITY).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC SWISS-2DPAGE: P99025; MOUSE.  
 DT INIT MET 0  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKIS 6  
 ||  
 Db 3 LLIS 6

## RESULT 4

UF01\_MOUSE  
 ID UF01\_MOUSE STANDARD; PRT; 5 AA.  
 AC P38639;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.D., He C., Selkirk J.K.;  
 RC "Separation and sequencing of familiar and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.  
 FT NON TER 5  
 SQ SEQUENCE 5 AA; 717 MW; 7364087C4310C000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7  
 ||  
 Db 2 IGR 4

## RESULT 5

UNC6\_CLOPA  
 ID UNC6\_CLOPA STANDARD; PRT; 6 AA.  
 AC P81351;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 6 from 2D-page (Fragment).  
 OS Clostridium pasteurianum.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 CC NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=96291870; PubMed=9629312;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.  
 FT NON TER 6  
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKI 5  
 ||  
 Db 3 TAEI 6

## RESULT 6

CCF1\_ENTFA  
 ID CCF1\_ENTFA STANDARD; PRT; 7 AA.  
 AC P20104;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone cCF10.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=89008313; PubMed=3139658;  
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
 RA Adsit J.C., Dunny G.M., Suzuki A.;  
 RT "Structure of cCF10, a peptide sex pheromone which induces  
 RT conjugative transfer of the Streptococcus faecalis tetracycline  
 RT resistance plasmid, pCF10.";

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RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: CFC IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR; A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 7209D2C731B2C74C CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 3 TL 4

RESULT 7
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID CHOX_ALCSP
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1983).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Oxidoreductase.
FT NON_TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
Db 6 SR 7

RESULT 8
CIA_ENTFA STANDARD; PRT; 7 AA.
ID CIA_ENTFA
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.

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CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BD072059CC5D80 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 3 FIL 5

RESULT 9
UC24_MAIZE STANDARD; PRT; 7 AA.
ID UC24_MAIZE
AC P80630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RX TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernolet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.
DR Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 665 MW; 6DC1S5B33DC1B5D0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLX 4
Db 2 TAK 4

RESULT 10
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the

```

RT allatostatin superfamily in the shore crab *Carcinus maenas*.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 5  
 FT SEQUENCE 5 AA; 586 MW; 672879D5AB30000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 Db 3 FGL 5

RESULT 11  
 PSK\_DAUCA  
 ID ALL2\_CARMA STANDARD; PRT; 5 AA.  
 AC P58261;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].  
 DE Daucus carota (Carrot).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.  
 CX NCBI\_TaxID=4039;  
 RN [1]

RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
 RC STRAIN=cv. US-Harumakigoesun;  
 RX MEDLINE=20212743; PubMed=10750705;  
 RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,  
 RA Kamada H., Sakagami Y.;  
 RT "A secreted peptide growth factor, phytosulfokine, acting as a  
 RT stimulatory factor of carrot somatic embryo formation.";  
 RL Plant Cell Physiol. 41:27-32 (2000).  
 CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
 CC EMBRYOS.

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
 CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
 KW Growth factor; Sulfation.

FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.  
 FT MOD\_RES 1 1 SULFATION.  
 FT MOD\_RES 3 3 SULFATION.  
 SQ SEQUENCE 5 AA; 487 MW; 76C15E504B30000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTL 2  
 Db 3 YL 4

RESULT 12  
 ALL2\_CARMA  
 ID ALL2\_CARMA STANDARD; PRT; 7 AA.  
 AC P81805;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 2.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 7  
 FT SEQUENCE 7 AA; 770 MW; 672879CDCB5DB70 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 Db 5 FGL 7

RESULT 13  
 ALL3\_CARMA  
 ID ALL3\_CARMA STANDARD; PRT; 7 AA.  
 AC P81806;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 3.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Multigene family.

SQ SEQUENCE 7 AA; 796 MW; 672879CDCB5DB70 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
 Db 5 FGL 7

RESULT 14  
 ALL4\_CARMA  
 ID ALL4\_CARMA STANDARD; PRT; 7 AA.  
 AC P81807;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 4.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

CC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476420 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
| |  
Db 5 FGL 7

RESULT 15  
ALL5 CARMA  
ID -ALL5\_CARMA STANDARD; PRT; 7 AA.  
AC P81808;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 5.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 7  
FT 7 AMIDATION  
SQ SEQUENCE 7 AA; 791 MW; 672879CDCB476420 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
| |  
Db 5 FGL 7

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 ; Search time 48 seconds  
(without alignments)  
37.633 Million cell updates/sec

Title: US-09-712-819C-6  
Perfect score: 35  
Sequence: 1 FTLKISR 7

Scoring table: ELCSJM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13	39.4	6	P82181	P82181 spinacia ol
2	13	39.4	6	P82182	P82182 spinacia ol
3	11	33.3	7	Q95945	Q95945 saccharomyc
4	10	30.3	6	P82541	P82541 spinacia ol
5	9	27.3	4	Q08433	Q08433 rattus sp.
6	9	27.3	7	O07354	O07354 syzechococc
7	9	27.3	7	Q8GL12	Q8GL12 borrelia bu
8	9	27.3	7	Q8GL04	Q8GL04 borrelia bu
9	9	27.3	7	Q8GL00	Q8GL00 borrelia bu
10	9	27.3	7	Q15897	Q15897 homo sapien
11	9	27.3	7	P93233	P93233 lycopersico
12	9	27.3	7	Q8K3H6	Q8K3H6 rattus norv
13	9	27.3	7	Q63480	Q63480 rattus norv
14	9	27.3	7	Q55184	Q55184 rattus norv
15	9	27.3	7	Q8JUE81	Q8JUE81 human immun
16	8	24.2	7	P70804	P70804 azotobacter

17	8	24.2	7	2	Q47029	Q47029 enterobacte
18	8	24.2	7	12	Q9YVE3	Q9YVE3 human: adenc
19	8	24.2	7	12	Q9YIQ9	Q9YIQ9 human: adenc
20	8	24.2	7	12	Q9YIR0	Q9YIR0 human: adenc
21	7	21.2	5	2	P83073	P83073 bacillus ce
22	7	21.2	7	2	P72081	P72081 nocardia la
23	7	21.2	7	4	Q8NH7	Q8NH7 homo sapien
24	7	21.2	7	12	Q66205	Q66205 transmissib
25	7	21.2	7	12	Q9YQ:0	Q9YQ:0 transmissib
26	6	18.2	5	13	P83308	P83308 gallus gall
27	6	18.2	7	2	O53556	O53556 actinobacil
28	6	18.2	7	2	Q54248	Q54248 streptomyce
29	6	18.2	7	2	Q8KMS9	Q8KMS9 enterobacte
30	6	18.2	7	2	C34028	C34028 sphingomora
31	6	18.2	7	4	C15903	C15903 homo sapien
32	6	18.2	7	6	Q28742	Q28742 oryctolagus
33	6	18.2	7	8	P92214	P92214 arabidopyrum
34	6	18.2	7	8	P92393	P92393 hordeum vul
35	6	18.2	7	8	P92403	P92403 lophopyrum
36	6	18.2	7	8	P92427	P92427 peridictyon
37	6	18.2	7	8	P92430	P92430 aegilops ta
38	6	18.2	7	9	P92221	P92221 bromus iner
39	6	18.2	7	8	C98866	C98866 spiracia ol
40	6	18.2	7	8	P92425	P92425 pseudoroegn
41	6	18.2	7	8	P92381	P92381 hordeum bra
42	6	18.2	7	8	P92387	P92387 horardia p
43	6	18.2	7	8	P92210	P92210 agropyron c
44	6	18.2	7	8	P92440	P92440 thinopyrum
45	6	18.2	7	8	P92218	P92218 australiopyr

ALIGNMENTS

RESULT 1

P82181  
ID P82181 PRELIMINARY; PRT; 6 AA.  
AC P82181;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
CX NCBI\_TaxID=3562;  
RN 11  
RP SEQUENCE.  
RC STRAIN=cv. ALVARO; TISSUE=leaf;  
RX MEDLINE=20435798; PubMed=10874046;  
RA Yamaguchi K., Subramanian A.R.;  
RT "The plastid ribosomal proteins. Identification of all the proteins in  
the 50 S subunit of an organelle ribosome (chloroplast).";  
RL J. Biol. Chem. 275:28466-28482(2000).  
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
DR InterPro; IPR001790; Ribosomal\_L10.  
DR InterPro; IPR002363; Ribosomal\_L10eub.  
DR Pfam; PF00466; Ribosomal\_L10; PARTIAL.  
DR PROSITE; PS01109; RIBOSOMAL\_L10; PARTIAL.  
KW Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7

```
Db      2 ISR 4
!!!
RESULT 2
P82182  PRELIMINARY;      PRT;      6 AA.
ID      P82182
AC      P82182;
DT      01-JUN-2000 (TrEMBLrel. 14, Last sequence update);
DT      01-JUN-2000 (TrEMBLrel. 14, Last sequence update);
DE      01-JUN-2002 (TrEMBLrel. 20, Last annotation update)
DE      Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS      Spinacia oleracea (Spinach).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX      NCBI_TaxID=3562;
RN      [1];
RP      SEQUENCE.
RC      STRAIN=cv. ALVARO; TISSUE=leaf;
RX      MEDLINE=20435798; PubMed=10874039;
RA      Yamaguchi K., Subramanian A.R.;
RT      "The plastid ribosomal proteins. Identification of all the proteins in
RT      the 50 S subunit of an organelle ribosome (chloroplast).";
RL      J. Biol. Chem. 275:28466-28492(2000).
CC      -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC      -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC      -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC      -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC      -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR      InterPro; IPR001790; Ribosomal_L10.
DR      Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR      PROSITE; PS01103; RIBOSOMAL_L10; PARTIAL.
KW      Ribosomal protein; Chloroplast; rRNA-binding.
FT      NON TER
SQ      SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match      39.4%; Score 13; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ISR 7
!!!
DB      2 ISR 4

RESULT 3
Q95945  PRELIMINARY;      PRT;      7 AA.
ID      Q95945
AC      Q95945;
DT      01-FEB-1997 (TrEMBLrel. 02, Created);
DT      01-FEB-1997 (TrEMBLrel. 02, Last sequence update);
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE      Inside intron 5 (Fragment).
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Mitochondrion.
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RN      [1];
RP      SEQUENCE FROM N.A.
RC      STRAIN=D273-10B;
RX      MEDLINE=81069885; PubMed=6254986;
RA      Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT      "Assembly of the mitochondrial membrane system: Structure and
RT      nucleotide sequence of the gene coding for subunit 1 of yeast
RT      cytochrome oxidase.";
RL      J. Biol. Chem. 255:11927-11941(1980).
DR      EMBL; V00694; CAA24066.1; -.
KW      Mitochondrion.
FT      NON TER
SQ      SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match      30.3%; Score 10; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLK 4
!!!
DB      3 SLK 5

RESULT 5
Q08433  PRELIMINARY;      PRT;      4 AA.
ID      Q08433
AC      Q08433;
DT      01-NOV-1996 (TrEMBLrel. 01, Created);
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE      Bilirubin UDP-glucuronosyltransferase (Fragment).
OS      Rattus sp.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX      NCBI_TaxID=10118;
RN      [1];
RP      SEQUENCE FROM N.A.
RC      STRAIN=Gunn;
```

RX MEDLINE=91282758; PubMed=1640486;  
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
hyperbilirubinemic Gunn rat.";  
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).  
DR EMBL; S38636; AAB19259.1; -.  
KW Transferase.  
FT NON TER 1  
SQ SEQUENCE 4 AA; 473 MW; 633732C423000000 CRC64;

Query Match 27.3%; Score 9; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
DB 3 LK 4

RESULT 6  
O07354  
ID O07354 PRELIMINARY; PRT; 7 AA.  
AC O07354;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created);  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update);  
DT 01-DEC-2002 (TrEMBLrel. 19, Last annotation update);  
DE NifK (Fragment).  
GN NIFK.  
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanotheca PCC 8801).  
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothaceae.  
OX NCBI\_TaxID=41431;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RF-1;  
RX MEDLINE=99231861; PubMed=10217509;  
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;  
RT "Organization and expression of nitrogen-fixation genes in the aerobic  
nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain  
RF-1.";  
RL Microbiology 145:743-753 (1999).  
DR EMBL; AF003700; AAC35193.1; -.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3  
DB 3 FDL 5

RESULT 7  
O8GL12  
ID O8GL12 PRELIMINARY; PRT; 7 AA.  
AC O8GL12;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);  
DE PF-50 protein (Fragment).  
GN PF-50.  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-9.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N40;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY142100; AAN17911.1; -.  
KW Plasmid.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
DB 6 LK 7

RESULT 8  
O8GL04  
ID O8GL04 PRELIMINARY; PRT; 7 AA.  
AC O8GL04;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);  
DE PF-50 protein (Fragment).  
GN PF-50.  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-5.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=93-0107;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142103; AAN17848.1; -.  
KW Plasmid.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
DB 6 LK 7

RESULT 9  
O8GL00  
ID O8GL00 PRELIMINARY; PRT; 7 AA.  
AC O8GL00;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);  
DE PF-50 protein (Fragment).  
GN PF-50.  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-13.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA15;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142106; AAN17857.1; -.  
KW Plasmid.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;



Query Match 27.3%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
||  
Db 6 LK 7

## RESULT 10

Q15897 Q15897 PRELIMINARY; PRT; 7 AA.  
AC Q15897;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE (Clone XP6A11A) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch E., Xiong M.,  
RA Coolbaugh M.I., Chinnait C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32077; AAA73887.1; -.  
FT NON\_TER 7  
FT SEQUENCE 7 AA; 814 MW; 672B1DD3372346B0 CRC64;  
SQ

Query Match 27.3%; Score 9; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
||  
Db 3 LK 4

## RESULT 11

P93233 P93233 PRELIMINARY; PRT; 7 AA.  
AC P93233;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14;  
DE (Fragment).  
GN LE-ACS1B.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97351561; PubMed=9207843;  
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;  
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
RT synthase genes by elicitor in suspension cultures of tomato  
RT (Lycopersicon esculentum).";  
RL Plant Mol. Biol. 34:275-286(1997).  
DR EMBL; U75692; AAC49682.1; -.  
KW Lyase.  
FT NON\_TER 1  
FT SEQUENCE 7 AA; 828 MW; 7-B412C7377435D0 CRC64;  
SQ

Query Match 27.3%; Score 9; DB 10; Length 7;

QY 4 KI 5

Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7  
||  
Db 1 SR 2

## RESULT 12

Q8K3H6 Q8K3H6 PRELIMINARY; PRT; 7 AA.  
AC Q8K3H6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Collagenase-3 (Fragment).  
GN MMP13.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Prietto S.M., Lyons J.G.;  
RT "Intron 1 of Rattus norvegicus MMP13";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY101357; AAM51172.1; -.  
FT NON\_TER 1  
FT NON\_TER 7  
FT SEQUENCE 7 AA; 907 MW; 63373B51EB1DD9A0 CRC64;  
SQ

Query Match 27.3%; Score 9; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4  
||  
Db 6 LK 7

## RESULT 13

Q63480 Q63480 PRELIMINARY; PRT; 7 AA.  
AC Q63480;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE TR4-NS orphan receptor (Fragment).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
RT of novel sequences in the 5'-untranslated region and C-terminal  
RT domain";  
RL Endocrinology 137:1562-1571(1996).  
DR EMBL; U59125; AAB02827.1; -.  
KW Receptor.  
FT NON\_TER 1  
FT SEQUENCE 7 AA; 758 MW; 672AA878640C5350 CRC64;  
SQ

Query Match 27.3%; Score 9; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 KI 2  
Query Match 27.3%; Score 9; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cyt 2 TL 3  
Db 4 TL 5  
Search completed: October 4, 2003, 12:48:32  
Job time : 48 secs

RESULT 14  
O55184  
ID O55184 PRELIMINARY; PRT; 7 AA.  
AC O55184;  
DT 01-JUN-1998 (TrEMBLrel. 26, Created)  
DT 01-JUN-1998 (TrEMBLrel. 26, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Orphan receptor TR4-NS (Fragment).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Scuriograthi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Dupont B.R., Leach R.C., Detera-Wadleigh S.D.;  
RA Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
of novel sequences in the 5'-untranslated region and C-terminal  
domain."  
RL Endocrinology 137:1562-1571(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96299786; PubMed=8661150;  
RA Yoshikawa T., Dupont B.R., Leach R.C., Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
expression and chromosomal localization of the human gene."  
RL Genomics 35:361-366(1996).  
DR EMBL; U59454; AAB31433.1; -.  
KW Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 563 MW; 60DAA8787E3C535C CRC64;

Query Match 27.3%; Score 9; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cyt 4 KI 5  
Db 1 KI 2

RESULT 15  
O8JE81  
ID O8JE81 PRELIMINARY; PRT; 7 AA.  
AC O8JE81;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN POL.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=4874;  
RX MEDLINE=22056123; PubMed=12060770;  
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
RA Hoffmann D., Korn K., Selbig J.;  
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics  
approach to predicting phenotype from genotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).  
DR EMBL; AF347267; AAK32344.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 985 MW; 76C37731A046C70C CRC64;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:26:27 ; Search time 51.6667 Seconds  
(without alignments)  
21.505 Million cell updates/sec

Title: US-09-712-819C-6  
Perfect score: 33  
Sequence: 1 FTLKISR 7

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 153726573 residues

Total number of hits satisfying chosen parameters: 76613

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:  
1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:  
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:  
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:  
4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:  
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6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:  
7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:  
8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:  
9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:  
10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:  
11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:  
12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:  
13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:  
14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:  
15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:  
16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:  
17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:  
18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:  
19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:  
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21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:  
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:  
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:  
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	59.7	7	20	AAY40736 S4 derivative #10,
2	23	69.7	7	21	AAB30074 Scaffold protein S
3	22	66.7	7	20	AAY40738 S4 derivative #12,
4	22	66.7	7	21	AAB30076 Scaffold protein S
5	21	63.6	7	20	AAY42013 Rheumatoid arthritis
6	20	60.6	7	16	AAR81848 Human afamin: trypt
7	20	60.6	7	20	AA418829 Rheumatoid arthritis
8	20	60.6	7	22	ABB55870 Vascular dementia-
9	20	60.6	7	22	ABB55981 Vascular dementia-

10	20	60.6	7	22	ABB56283 Vascular dementia-
11	20	60.6	7	22	ABB52190 Human API-146 tryp
12	20	60.6	7	22	ABB52355 Human API-125 tryp
13	20	60.6	7	22	AAU28602 DPI tryptic digest
14	20	60.6	7	22	AAU24969 Schizophrenia-Asso
15	20	60.6	7	22	AAU26249 Depression-Asso
16	20	60.6	7	22	AAU15313 Schizophrenia-asso
17	20	60.6	7	23	ABG78730 Multiple sclerosis
18	20	60.6	7	23	ABG78901 Multiple sclerosis
19	20	60.6	7	24	ABP57283 Breast cancer asso
20	20	60.6	7	24	ABP57255 Breast cancer asso
21	20	60.6	7	24	ABP58010 Prostate cancer ma
22	19	57.6	7	20	AA40737 S4 derivative #11,
23	19	57.6	7	21	AAB30075 Scaffold protein S
24	18	54.5	7	23	ABR40481 Human secreted pro
25	18	54.5	7	23	ABP66518 Human RSV antibody
26	18	54.5	7	23	ABB81854 Staphylococcus aur
27	18	54.5	7	24	ABU69381 Respiratory syncyt
28	17	51.5	6	20	AAW84431 HIV-1 nucleic acid
29	17	51.5	6	23	AAE28110 Human immunoglobul
30	17	51.5	6	24	ABP95994 Microtetraspora re
31	17	51.5	7	11	AAR07656 Ribonuclease reduc
32	17	51.5	7	17	AAR97970 Antigenic fragment
33	17	51.5	7	19	AAW69249 Haemagglutinin hea
34	17	51.5	7	23	ABE66439 Human RSV antibody
35	17	51.5	7	24	ABU69352 Respiratory syncyt
36	16	48.5	5	16	AAR75584 SPI20 binding Fab
37	16	48.5	6	10	AAP93345 Portion of myc var
38	16	48.5	6	18	AAW39453 Human T cell epito
39	16	48.5	6	20	AA40736 TATA box recognizi
40	16	48.5	6	21	AAB38999 Human secreted pep
41	16	48.5	6	22	AAG63074 A Hepatitis A viru
42	16	48.5	6	23	AAE28096 Human immunoglobul
43	16	48.5	6	23	ABJ11455 Human 125P5C8 epit
44	16	48.5	6	24	ABR44950 Staphylococcus aur
45	16	48.5	6	24	ABR45342 Staphylococcus aur

ALIGNMENTS

RESULT 1

AA40736  
ID AA40736 standard; peptide; 7 AA.

XX AA40736;

AC AA40736;

DT 01-DEC-1999 (first entry)

XX S4 derivative #10, beta strand of scaffold protein structure.

DE S4 derivative #10, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;

KW tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

PF 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

PA Desmet J, Hufton S, Hoogenboom H, Sablon E;

PI WPI; 1999-542958/46.

DR New scaffold protein, useful for stabilizing antigens used as vaccines

XX

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a

CC cytotoxic molecule or an autoimmune antibody which may then kill the

CC tumour cells. Therefore the scaffold protein may be used to target

CC chemotherapeutic agents to specific cells. It may also be used to

CC stabilize individual peptides in a peptide library and may be used in

CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

SQ Query Match 59.7%; Score 23; DB 20; Length 7;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKIS 6

Db 2 FTLSSIS 7

RESULT 2

AAB30074

ID AAB30074 standard; Peptide; 7 AA.

XX

AC AAB30074;

XX

DT 09-FEB-2001 (first entry)

XX

DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.

XX

XW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;

XW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;

XW diabetic retinopathy; atherosclerosis.

XX

OS Synthetic.

XX WC2000060070-A1.

PN 12-OCT-2000.

XX

PD 01-APR-1999; 99WO-EP02283.

XX

PR 01-APR-1999; 99WO-EP02283.

XX

PA (INNO-) INNOGENETICS NV.

XX

Pi Desmet J, Hufton S, Hoogenboom H, Sahlon E;

XX

DR WPI; 2000-665002/64.

XX

XX Scaffold composed of single-chain polypeptide having beta sandwich

PT architecture carrying new and randomized peptide sequences useful as

PT supporting framework and carrying antigen- or receptor binding

PT fragments

XX

PS Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins

CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be

CC used as a scaffold to bind antigen- or receptor-binding fragments. These

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

XX Query Match 69.7%; Score 23; DB 21; Length 7;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKIS 6

Db 2 FTLSSIS 7

RESULT 3

AAY40738

ID AAY40738 standard; peptide; 7 AA.

XX

AC AAY40738;

XX

DT 01-DEC-1999 (first entry)

XX

DE S4 derivative #12, beta strand of scaffold protein structure.

XX

XW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;

XW tumour; chemotherapeutic agent.

XX

OS Synthetic.

XX EP947582-A1.

PN 06-OCT-1999.

XX

PD 31-MAR-1998; 98EP-0870065.

XX

PR 31-MAR-1998; 98EP-0870065.

XX

PA (INNO-) INNOGENETICS NV.

XX

Pi Desmet J, Hufton S, Hoogenboom H, Sahlon E;

XX

DR WPI; 1999-542958/46.

XX

PT New scaffold protein, useful for stabilizing antigens used as vaccines

XX

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a  
CC cytotoxic molecule or an autoimmune antibody which may then kill the  
CC tumour cells. Therefore the scaffold protein may be used to target  
CC chemotherapeutic agents to specific cells. It may also be used to  
CC stabilize individual peptides in a peptide library and may be used in  
CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 66.7%; Score 22; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6  
|||  
Db 2 FLTKIS 7

RESULT 4  
AAB30076  
ID AAB30076 standard; Peptide; 7 AA.

XX AAB30076;

DT 09-FEB-2001 (first entry)

DE Scaffold protein SCA S4 peptide SEQ ID NO: 137.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
KW diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WO200060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WO-EP02283.

XX 01-APR-1999; 99WO-EP02283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich  
PT architecture carrying new and randomized peptide sequences useful as  
PT supporting framework and carrying antigen- or receptor binding  
PT fragments.

XX Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins  
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be  
CC used as a scaffold to bind antigen- or receptor-binding fragments. These  
CC can be used in the treatment of diseases such as cancer,  
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and  
CC diabetic retinopathy. Sequences AAB29930-B29939 were used in the  
CC production of the proteins of the invention.

XX Sequence 7 AA;

Query Match 66.7%; Score 22; DB 21; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6  
|||  
Db 2 FLTKIS 7

RESULT 5  
AAY42013  
ID AAY42013 standard; Peptide; 7 AA.

XX AAY42013;

DT 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #164.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;  
KW rheumatoid arthritis diagnostic feature; ERI; synovial fluid;  
KW rheumatoid arthritis diagnostic protein isoform; screening;  
KW expression reference protein isoform; prognosis.

XX Homo sapiens.

XX WC9947925-A2.

XX 23-SEP-1999.

XX 15-MAR-1999; 99WO-GB00763.

XX 13-MAR-1998; 98GB-0005477.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Parekh RB, Patel TP, Townsend RR;

XX WPI; 1999-571871/48.

XX Diagnosis of human rheumatoid arthritis by two-dimensional  
PT electrophoresis -

XX Disclosure; Page 21; 157pp; English.

XX A method has been developed for the diagnosis of human rheumatoid  
CC arthritis (RA) using two-dimensional electrophoresis to generate a  
CC two-dimensional array of features. The method can be used for screening,  
CC diagnosis and prognosis of RA in a subject or for monitoring the effect  
CC of an anti-RA drug or therapy administered to a subject. The method  
CC comprises: (a) analysing a sample of serum or plasma and optionally  
CC synovial fluid by two-dimensional electrophoresis, to generate a two-  
CC dimensional array of features; (b) identifying at least one chosen  
CC feature whose relative abundance correlates with the presence or absence  
CC of RA; and (c) comparing the abundance of each chosen feature in the  
CC sample with the abundance of that chosen feature in serum or plasma from  
CC one or more persons without RA, where the relative abundance of the  
CC chosen feature or features in the sample indicates the presence or  
CC absence of RA in the subject. The method can also be used in clinical  
CC studies for testing drugs for therapy of RA, for purification of RA-  
CC diagnostic protein isoforms (RPIs), and for production of antibodies to  
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify  
CC compounds that promote or inhibit their activity, which are then used as  
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy  
CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to  
CC AAY42103 represent expression reference protein isoform peptides and  
CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all  
CC used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 63.6%; Score 21; DB 20; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKISR 7  
!|  
Db 2 TLMISR 7

RESULT 6

AAR81848  
ID AAR81848 standard; peptide; 7 AA.  
XX  
AC AAR81848;  
XX  
DT 16-MAY-1996 (first entry)  
XX  
DE Human afamin tryptic fragment FX20.  
XX  
KW Human; afamin; serum protein family; albumin; alpha-fetoprotein; plasma;  
KW vitamin D binding protein; homology; post-translational processing;  
KW chromatography; primer; PCR; amplification; probe; rheumatoid arthritis;  
KW ischaemia-reperfusion injury; ARDS; cardiopulmonary bypass; sepsis;  
KW toxic plasma substance; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO9527059-A1.  
XX  
PD 12-OCT-1995.  
XX  
PF 31-MAR-1995; 95WO-US04075.  
XX  
PR 31-MAR-1994; 94US-0222619.  
XX  
PA (AMGE-) AMGEN INC.  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Lichenstein HS, Lyons DE, Wright SD, Wurfel XM;  
XX  
DR WPI; 1995-358634/46.  
XX  
PT Human afamin or a variant and polynucleotide(s) encoding it - a  
PT human serum protein with activities in common with other members of  
PT this family.  
XX  
PS Example 3; Page 45; 97pp; English.  
XX  
CC Peptides AAR81847-54 are tryptic peptide fragments from human afamin  
CC (AAR81845) novel member of the human serum protein family. The  
CC fragments were used to design primers and probes (AATC3786-38) for the  
CC cloning of the afamin gene (AATC3785) from human liver cDNA. Afamin is  
CC thought to have similar properties to human albumin, alpha-fetoprotein  
CC and vitamin D binding protein due to homology with these proteins. The  
CC gene encodes a mature protein of 66576 daltons without post-translational  
CC processing (ca. 97000 daltons with post-translational processing). The  
CC protein was isolated from human plasma by a conventional chromatographic  
CC methods. The protein can be used to ameliorate ischaemia-reperfusion  
CC injury, rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic  
CC plasma substances released after inflammation, etc.  
XX  
SQ Sequence 7 AA;  
Query Match: 50.6%; Score 20; FR 16; Length 7;  
Best Local Similarity 57.1%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
|||  
Db 1 FTFEYSR 7

RESULT 7  
AAY41889  
ID AAY41889 standard; Peptide; 7 AA.  
XX  
AC AAY41889;  
XX  
DT 09-DEC-1999 (first entry)  
XX  
DE Rheumatoid arthritis diagnostic protein isoform peptide #40.  
XX  
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;  
KW rheumatoid arthritis diagnostic protein isoform; screening;  
KW expression reference protein isoform; prognosis.  
XX  
OS Homo sapiens.  
XX  
PN WO9947925-A2.  
XX  
PD 23-SEP-1999.  
XX  
PF 15-MAR-1999; 99WO-GB00763.  
XX  
PR 13-MAR-1998; 98GB-0005477.  
XX  
PA (OXPC-) OXFORD GLYCOSCIENCES JK LTD.  
XX  
PI Parekh RB, Patel TP, Townsend RR;  
XX  
DR WPI; 1999-571871/46.  
XX  
PT Diagnosis of human rheumatoid arthritis by two-dimensional  
PT electrophoresis -  
XX  
PS Disclosure; Page 18; 157pp; English.  
XX  
CC A method has been developed for the diagnosis of human rheumatoid  
CC arthritis (RA) using two-dimensional electrophoresis to generate a  
CC two-dimensional array of features. The method can be used for screening,  
CC diagnosis and prognosis of RA in a subject or for monitoring the effect  
CC of an anti-RA drug or therapy administered to a subject. The method  
CC comprises: (a) analysing a sample of serum or plasma and optionally  
CC synovial fluid by two-dimensional electrophoresis, to generate a two-  
CC dimensional array of features; (b) identifying at least one chosen  
CC feature whose relative abundance correlates with the presence or absence  
CC of RA; and (c) comparing the abundance of each chosen feature in the  
CC sample with the abundance of that chosen feature in serum or plasma from  
CC one or more persons without RA, where the relative abundance of the  
CC chosen feature or features in the sample indicates the presence or  
CC absence of RA in the subject. The method can also be used in clinical  
CC studies for testing drugs for therapy of RA, for purification of RA-  
CC diagnostic protein isoforms (RPIs), and for production of antibodies to  
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify  
CC compounds that promote or inhibit their activity, which are then used as  
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy  
CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to  
CC AAY42103 represent expression reference protein isoform peptides and  
CC AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
Query Match: 60.6%; Score 20; DB 20; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
|||  
Db 1 YTFELSR 7

RESULT 8  
ABB55870  
ID ABB55870 standard; Peptide; 7 AA.  
XX  
AC ABB55870;  
XX  
DT 15-FEB-2002 (first entry)  
XX  
DE Vascular dementia-associated protein isoform (VPI) 70.  
XX  
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;  
KW diagnosis; prognosis; gene therapy.  
XX

```
OS Homo sapiens.
XX WO200169261-A2.
XX 20-SEP-2001.
XX 14-MAR-2001; 2001WO-GB01106.
XX 15-MAR-2000; 2000GB-0006285.
XX 24-NOV-2000; 2000GB-0028734.
XX 28-NOV-2000; 2000US-0724391.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA
XX PI Herath HMAC, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
XX determining stage of VD and monitoring the effect of VD therapy,
XX comprises analysing body fluid by 2-dimensional electrophoresis for
XX features correlated with VD.
XX Claim 6; Page 31; 151pp; English.
XX The invention relates to screening, diagnosis or prognosis of Vascular
XX Dementia (VD) in a subject comprising analysing body fluid from the
XX subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
XX features containing at least one chosen feature whose relative abundance
XX correlates with the presence, absence, stage or severity of VD or
XX predicts the onset or course of VD, especially detecting in a sample of
XX cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
XX protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
XX specification. Detecting VD-associated features and VPI is useful for the
XX screening, diagnosis or prognosis of VD, for determining the stage or
XX severity of VD, for identifying a subject at risk of VD or for
XX monitoring the effect of therapy administered to a subject having VD.
XX Nucleic acids encoding a VPI or inhibiting the function of a VPI are
XX useful for the treatment of VD and for gene therapy.
XX Sequence 7 AA;
SQ
Query Match 60.6%; Score 20; DB 22; Length 7;
Best Local Similarity 42.9%; Pred. No. 9.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 FTLKISR 7
DB 1 YTFELSR 7
RESULT 9
ABB55981
ID ABB55981 standard; Peptide; 7 AA.
XX AC ABB55981;
XX 15-FEB-2002 (first entry)
XX Vascular dementia-associated protein isoform (VPI) 181.
XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX diagnosis; prognosis; gene therapy.
XX Homo sapiens.
XX WO200169261-A2.
XX 20-SEP-2001.
XX 14-MAR-2001; 2001WO-GB01106.
XX 15-MAR-2000; 2000GB-0006285.
PR 24-NOV-2000; 2000GB-0028734.
XX 28-NOV-2000; 2000US-0724391.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA
XX PI Herath HMAC, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
XX determining stage of VD and monitoring the effect of VD therapy,
XX comprises analysing body fluid by 2-dimensional electrophoresis for
XX features correlated with VD.
XX Claim 6; Page 33; 151pp; English.
XX The invention relates to screening, diagnosis or prognosis of Vascular
XX Dementia (VD) in a subject comprising analysing body fluid from the
XX subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
XX features containing at least one chosen feature whose relative abundance
XX correlates with the presence, absence, stage or severity of VD or
XX predicts the onset or course of VD, especially detecting in a sample of
XX cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
XX protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
XX specification. Detecting VD-associated features and VPI is useful for the
XX screening, diagnosis or prognosis of VD, for determining the stage or
XX severity of VD, for identifying a subject at risk of VD or for
XX monitoring the effect of therapy administered to a subject having VD.
XX Nucleic acids encoding a VPI or inhibiting the function of a VPI are
XX useful for the treatment of VD and for gene therapy.
XX Sequence 7 AA;
SQ
Query Match 60.6%; Score 20; DB 22; Length 7;
Best Local Similarity 42.9%; Pred. No. 9.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 FTLKISR 7
DB 1 YTFELSR 7
RESULT 10
ABB56283
ID ABB56283 standard; Peptide; 7 AA.
XX AC ABB56283;
XX 15-FEB-2002 (first entry)
XX Vascular dementia-associated protein isoform (VPI) 483.
XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX diagnosis; prognosis; gene therapy.
XX Homo sapiens.
XX WO200169261-A2.
XX 20-SEP-2001.
XX 14-MAR-2001; 2001WO-GB01106.
XX 15-MAR-2000; 2000GB-0006285.
XX 24-NOV-2000; 2000GB-0028734.
XX 28-NOV-2000; 2000US-0724391.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA
XX PI Herath HMAC, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX
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PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for  
PT determining stage of VD and monitoring the effect of VD therapy, for  
PT comprises analysing body fluid by 2-dimensional electrophoresis for  
PT features correlated with VD -  
XX  
PS Claim 6; Page 40; 151pp; English.  
XX  
CC The invention relates to screening, diagnosis or prognosis of vascular  
CC dementia (VD) in a subject comprising analysing body fluid from the  
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of  
CC features containing at least one chosen feature whose relative abundance  
CC correlates with the presence, absence, stage or severity of VD or  
CC predicts the onset or course of VD, especially detecting in a sample of  
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated  
CC protein isoforms (VPIs) (ABB5801-ABB56295) as fully defined in the  
CC specification. Detecting VD-associated features and VPI is useful for the  
CC screening, diagnosis or prognosis of VD, for determining the stage or  
CC severity of VD, for identifying a subject at risk of VD or for  
CC monitoring the effect of therapy administered to a subject having VD.  
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are  
CC useful for the treatment of VD and for gene therapy.  
XX  
SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
||:|  
Db 1 YTFELSR 7

RESULT 11

ABB52190  
ID ABB52190 standard; Peptide; 7 AA.

XX ABB52190;

DT 08-FEB-2002 (first entry)

DE Human API-146 tryptic digest peptide #1.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;  
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;  
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;  
KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

XX WO200175454-A2.

PN 11-OCT-2001.

PF 03-APR-2001; 2001WO-US10908.

XX 03-APR-2000; 2000US-194504P.

PR 28-NOV-2000; 2000US-253647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA (PFIZ ) PFIZER INC.

XX Durham KL, Friedman DL, Herath HMA, Kimmei LH, Parekh RB;  
PI Potter DM, Rohlf C, Silber BV, Stiger TR, Sunderland PT;  
PI Townsend RR, White F, Williams SA;

XX WPI; 2001-639384/73.

XX Screening for Alzheimer's disease in a mammal, by making  
PT two-dimensional array of a feature whose relative abundance correlates  
PT with disease, and comparing with abundance of the feature in samples of  
PT healthy persons -

PS Example; Page 30; 162pp; English.  
XX The invention relates to methods for the screening, diagnosis and  
CC prognosis of Alzheimer's disease. The methods involve the detection  
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's  
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,  
CC serum or plasma. The abundance of the AFs and APIs is then  
CC normalised to an Expression Reference Protein Isoform (ERPI) in  
CC order to determine whether a patient is suffering from, or has  
CC a predisposition to, Alzheimer's Disease. The relative abundance of  
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.  
CC The present sequence is a peptide produced from an API by proteolysis.  
XX  
SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 57.1%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
||:|  
Db 1 FTFEYSR 7

RESULT 12

ABB52355  
ID ABB52355 standard; Peptide; 7 AA.

XX ABB52355;

DT 08-FEB-2002 (first entry)

DE Human API-125 tryptic digest peptide #8.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;  
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;  
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;  
KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

XX WO200175454-A2.

PN 11-OCT-2001.

PF 03-APR-2001; 2001WO-US10908.

XX 03-APR-2000; 2000US-194504P.

PR 28-NOV-2000; 2000US-253647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA (PFIZ ) PFIZER INC.

XX Durham KL, Friedman DL, Herath HMA, Kimmei LH, Parekh RB;  
PI Potter DM, Rohlf C, Silber BV, Stiger TR, Sunderland PT;  
PI Townsend RR, White F, Williams SA;

XX WPI; 2001-639384/73.

XX Screening for Alzheimer's disease in a mammal, by making  
PT two-dimensional array of a feature whose relative abundance correlates  
PT with disease, and comparing with abundance of the feature in samples of  
PT healthy persons -

PS Example; Page 34; 162pp; English.

XX The invention relates to methods for the screening, diagnosis and  
CC prognosis of Alzheimer's disease. The methods involve the detection  
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's  
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,  
CC serum or plasma. The abundance of the AFs and APIs is then  
CC normalised to an Expression Reference Protein Isoform (ERPI) in  
CC order to determine whether a patient is suffering from, or has



CC a predisposition to, Alzheimer's Disease. The relative abundance of  
CC the Afs and APIs correlates with the severity of Alzheimer's Disease.  
CC The present sequence is a peptide produced from an API by proteolysis.

XX  
SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
:|:|:  
Db 1 YTFELSR 7

RESULT 13

AAU28602  
ID AAU28602 standard; Peptide; 7 AA.

XX AC AAU28602;

XX DT 03-JAN-2002 (first entry)

DE DPI tryptic digest peptide #193.

XX Human; depression associated protein isoform; tryptic digest peptide;  
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
KW maniac-depressive illness; schizoaffective disorder.

XX OS Homo sapiens.

XX WO200162787-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WC-GB00786.

XX PR 24-FEB-2000; 2000GB-0004412.

XX PR 08-DEC-2000; 2000GB-0030050.

XX PR 12-DEC-2000; 2000US-0254830.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HYAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX DR WPI; 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective  
PT disorder, which is used for diagnosis, prophylaxis and therapy of  
PT neuropsychiatric disorders, such as bipolar affective disorder -

XX PS Disclosure; Page 34; 153pp; English.

XX The present invention relates to the identification of depression  
CC associated protein isoforms (DPIs), particularly the tryptic digest  
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
CC (bipolar affective disorder) subjects, whilst other DPIs  
CC (AAU28626-AAU2887) are increased in BAD subjects. Also described  
CC are peptide sequences identified from DPI-45 and DPI-213 and the  
CC nucleic acid sequence they are encoded by. The sequences of the  
CC invention are useful for clinical screening, diagnosis, prognosis,  
CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
CC attention deficit disorders, schizoaffective disorders, and unipolar  
CC affective disorders. The present sequence represents one of the DPI  
CC tryptic digest peptides of the present invention.

XX Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+05;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FTLKISR 7  
:|:|:  
Db 1 YTFELSR 7

RESULT 14

AAU24969

ID AAU24969 standard; Peptide; 7 AA.

XX AC AAU24969;

XX DT 18-DEC-2001 (first entry)

DE Schizophrenia-Associated Protein Isoform (SPI) peptide #196.

XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX OS Homo sapiens.

XX WO200162785-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB00792.

XX PR 24-FEB-2000; 2000GB-0004415.

XX PR 28-NOV-2000; 2000US-0750395.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HYAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX DR WPI; 2001-570624/64.

XX New schizophrenia associated protein isoforms and encoding nucleic acid  
PT molecules, useful for treatment, diagnosis and prognosis of  
PT schizophrenia and screening for potential drugs for treatment and new  
PT drug targets -  
XX PS Disclosure; Page 32; 148pp; English.

XX The sequence represents a schizophrenia-associated protein isoform (SPI).  
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
CC in cerebrospinal fluid, serum or plasma and are useful markers of  
CC schizophrenia. The sequences can be used for treatment and diagnosis of  
CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
CC identifying patients most likely to respond to a particular therapy and  
CC identification of new targets for drug treatment. SPI DNA is useful as a  
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
:|:|:  
Db 1 YTFELSR 7

RESULT 15

AAU26249

ID AAU26249 standard; Peptide; 7 AA.

XX AC AAU26249;

XX DT 18-DEC-2001 (first entry)

XX DE Depression-Associated Protein isoform DPI-208.

XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
KW attention deficient disorder; schizophrenia; neuroleptic;  
KW unipolar affective disorder;  
XX  
XX Homo sapiens.  
XX  
XX WO200163294-A2.  
XX  
XX 30-AUG-2001.  
XX  
XX 23-FEB-2001; 2001WO-GB00792.  
XX  
XX 24-FEB-2000; 2000GB-0004412.  
XX 08-DEC-2000; 2000GB-0030050.  
XX 12-DEC-2000; 2000US-0254830.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAc, Parekh RB, Rohlf C;  
XX WPI; 2001-582081/65.  
XX  
XX Preparation for diagnosing or treating bipolar affected disorder (BAD);  
PT or unipolar depression, or for screening for modulators, comprises a  
PT BAD-associated protein isoform.  
XX  
XX Claim 8; Page 34; 163pp; English.  
XX  
XX The invention relates to a preparation comprising an isolated Bipolar  
CC Affected Disorder (BAD)-Associated Protein Isoform (DPI). The DPI's are  
CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
CC determine the stage or severity of BAD or unipolar depression, identify a  
CC subject at risk of developing BAD or unipolar depression, or monitor the  
CC effect of therapy in a subject. They are also used to screen for or  
CC identify agents that interact with a DPI. These agents, antibodies  
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
CC or prevent BAD or unipolar depression. Diseases that can be treated are  
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
CC unipolar affective disorder. The DPIs are used in proteomics. The  
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
CC BAD or unipolar depression overcomes the problems of using gene  
CC expression analysis, such as not being able to obtain central nervous  
CC system (CNS) tissue from a living patient under normal circumstances.  
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
CC fluid) of subjects having BAD.  
XX  
XX SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;  
Best Local Similarity 42.9%; Pred. No. 9.3e+55;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
DB 1 YTFELSR 7

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Job time : 52.6667 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:48:43 ; Search time 33.6667 seconds  
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Title: US-09-712-819C-6  
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Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 587654 seqs, 159212981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	7	10	US-09-791-378-198 Sequence 198, App
2	20	60.6	7	10	US-09-998-909-7 Sequence 7, Appl
3	20	60.6	7	10	US-09-826-290-205 Sequence 205, App
4	20	60.6	7	10	US-09-826-290-370 Sequence 370, App
5	20	60.6	7	11	US-09-791-393-145 Sequence 145, App
6	20	60.6	7	11	US-09-791-389-145 Sequence 145, App
7	18	54.5	7	11	US-09-996-265-164 Sequence 164, App
8	18	54.5	7	11	US-09-996-265-164 Sequence 164, App
9	18	54.5	7	12	US-10-162-497-78 Sequence 78, Appl
10	17	51.5	6	15	US-10-105-930-39 Sequence 39, Appl
11	17	51.5	6	15	US-10-043-539-30 Sequence 30, Appl
12	17	51.5	7	10	US-09-996-288-135 Sequence 135, App
13	17	51.5	7	11	US-09-996-265-135 Sequence 135, App
14	17	51.5	7	14	US-10-044-034-13 Sequence 13, Appl
15	16	48.5	6	10	US-09-727-963A-88 Sequence 88, Appl

16	48.5	6	15	US-10-211-994-23	Sequence 23, Appl
17	48.5	7	9	US-09-989-789-396	Sequence 396, App
18	48.5	7	9	US-09-989-789-197	Sequence 197, Ap
19	48.5	7	9	US-09-989-789-3503	Sequence 3503, Ap
20	48.5	7	9	US-09-989-789-3542	Sequence 3542, Ap
21	48.5	7	9	US-09-989-789-3544	Sequence 3544, Ap
22	48.5	7	9	US-09-796-848A-20	Sequence 20, Appl
23	48.5	7	10	US-09-844-508-43	Sequence 43, Appl
24	48.5	7	10	US-09-808-387-44	Sequence 44, Appl
25	48.5	7	10	US-09-996-288-35	Sequence 35, Appl
26	48.5	7	10	US-09-996-288-96	Sequence 96, Appl
27	48.5	7	10	US-09-996-288-131	Sequence 131, App
28	48.5	7	11	US-09-990-186-396	Sequence 396, App
29	48.5	7	11	US-09-990-186-1971	Sequence 1971, Ap
30	48.5	7	11	US-09-990-186-3503	Sequence 3503, Ap
31	48.5	7	11	US-09-990-186-3542	Sequence 3542, Ap
32	48.5	7	11	US-09-990-186-3544	Sequence 3544, Ap
33	48.5	7	11	US-09-996-265-35	Sequence 35, Appl
34	48.5	7	11	US-09-996-265-96	Sequence 96, Appl
35	48.5	7	11	US-09-996-265-131	Sequence 131, App
36	48.5	7	11	US-09-989-994-396	Sequence 396, App
37	48.5	7	11	US-09-989-994-1971	Sequence 1971, Ap
38	48.5	7	11	US-09-989-994-3503	Sequence 3503, Ap
39	48.5	7	11	US-09-989-994-3542	Sequence 3542, Ap
40	48.5	7	11	US-09-989-994-3544	Sequence 3544, Ap
41	48.5	7	14	US-10-050-552A-4	Sequence 4, Appl
42	48.5	7	15	US-10-084-826-43	Sequence 43, Appl
43	48.5	7	15	US-10-234-026-6	Sequence 6, Appl
44	45.5	4	12	US-10-348-167-36	Sequence 36, Appl
45	45.5	5	12	US-10-286-186-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-791-378-198  
; Sequence 198, Application US/09791378  
; Patent No. US20020142303A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; FILE OF INVENTION: SCHIZOPHRENIA  
; FILE REFERENCE: 9195-061-999  
; CURRENT APPLICATION NUMBER: US/09/791,378  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 198  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-378-198

Query Match 60.6%; Score 20; DB 10; Length 7;  
Best Local Similarity 42.9%; Pred. NO. 5.2e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
:|:|:  
Dh 1 YTFELSR 7

RESULT 2  
US-09-998-909-7  
; Sequence 7, Application US/09998909  
; Patent No. US20020164664A1  
; GENERAL INFORMATION:  
; APPLICANT: Hlavaty, John  
; APPLICANT: Briggman, Joseph  
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer

FILE REFERENCE: MTP-027  
CURRENT APPLICATION NUMBER: US/09/999,909  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: US 60/250,284  
PRIOR FILING DATE: 2000-11-30  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-998-909-7

Query Match 60.6%; Score 20; DB 10; Length 7;  
Best Local Similarity 42.9%; Pred. No. 5.2e+05;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|| :||  
Db 1 YTFELSR 7

## RESULT 3

US-09-826-290-205  
Sequence 205, Application US/09826290  
Patent No. US20020164668A1  
GENERAL INFORMATION:

APPLICANT: Durham, L. Kathryn  
APPLICANT: Friedman, David L.  
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
APPLICANT: Kimmel, Lida H.  
APPLICANT: Parekh, Rajesh Bhikhu  
APPLICANT: Potter, David M.  
APPLICANT: Rohlf, Christian  
APPLICANT: Silber, B. Michael  
APPLICANT: Stiger, Thomas R.  
APPLICANT: Sunderland, P. Trey  
APPLICANT: Townsend, Robert Reid  
APPLICANT: White, Frost  
APPLICANT: Williams, Stephen A.

TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and  
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of  
TITLE OF INVENTION: Alzheimer's Disease

FILE REFERENCE: 2572-1-001 N2  
CURRENT APPLICATION NUMBER: US/09/826,290  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/194,504  
PRIOR FILING DATE: 2000-04-03  
PRIOR APPLICATION NUMBER: US 60/253,647  
PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 492  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 205  
LENGTH: 7  
TYPE: PRT  
ORGANISM: homo sapien  
US-09-826-290-205

Query Match 60.6%; Score 20; DB 10; Length 7;  
Best Local Similarity 57.1%; Pred. No. 5.2e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|| :||  
Db 1 FTPEYSR 7

## RESULT 4

US-09-826-290-370  
Sequence 370, Application US/09826290  
Patent No. US20020164668A1  
GENERAL INFORMATION:

APPLICANT: Durham, L. Kathryn

APPLICANT: Friedman, David L.  
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
APPLICANT: Kimmel, Lida H.  
APPLICANT: Parekh, Rajesh Bhikhu  
APPLICANT: Potter, David M.  
APPLICANT: Rohlf, Christian  
APPLICANT: Silber, B. Michael  
APPLICANT: Stiger, Thomas R.  
APPLICANT: Sunderland, P. Trey  
APPLICANT: Townsend, Robert Reid  
APPLICANT: White, Frost  
APPLICANT: Williams, Stephen A.

TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and  
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of  
TITLE OF INVENTION: Alzheimer's Disease

FILE REFERENCE: 2572-1-001 N2  
CURRENT APPLICATION NUMBER: US/09/826,290  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/194,504  
PRIOR FILING DATE: 2000-04-03  
PRIOR APPLICATION NUMBER: US 60/253,647  
PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 492  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 370  
LENGTH: 7  
TYPE: PRT  
ORGANISM: homo sapien  
US-09-826-290-370

Query Match 60.6%; Score 20; DB 10; Length 7;  
Best Local Similarity 42.9%; Pred. No. 5.2e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|| :||  
Db 1 YTFELSR 7

## RESULT 5

US-09-791-393-145  
Sequence 145, Application US/09791393  
Publication No. US20030032203A1  
GENERAL INFORMATION:

APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
APPLICANT: Parekh, Rajesh Bhikhu  
APPLICANT: Rohlf, Christian

TITLE OF INVENTION: Proteins, Genes and Their Use for  
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)

FILE REFERENCE: 2543-1-001 N1  
CURRENT APPLICATION NUMBER: US/09/791,393  
CURRENT FILING DATE: 2002-01-02  
EARLIER APPLICATION NUMBER: GB 0004412.3  
EARLIER FILING DATE: 2000-02-24  
EARLIER APPLICATION NUMBER: GB 0030050.9  
EARLIER FILING DATE: 2000-12-08  
EARLIER APPLICATION NUMBER: US 60/254,830  
EARLIER FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 308  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 145  
LENGTH: 7  
TYPE: PRT  
ORGANISM: homo sapien  
US-09-791-393-145

Query Match 60.6%; Score 20; DB 11; Length 7;  
Best Local Similarity 42.9%; Pred. No. 5.2e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7  
|| :||

Db 1 YTFELSR 7

## RESULT 6

US-09-791-389-145  
; Sequence 145, Application US/09791389  
; Publication No. US2003032773A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mediyanselage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-791-389-145

Query Match 60.6%; Score 20; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 5.2e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7

Db 1 YTFELSR 7

## RESULT 7

US-09-996-288-164  
; Sequence 164, Application US/09996288  
; Patent No. US2002017726A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 164  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-164

Query Match 54.5%; Score 18; DB 10; Length 7;  
Best Local Similarity 60.0%; Pred. No. 5.2e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKIS 6

Db 2 TMKLS 6

## RESULT 8

US-10-105-930-39

; Sequence 39, Application US/10105930

US-09-996-265-164  
; Sequence 164, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 164  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-164

Query Match 54.5%; Score 18; DB 11; Length 7;  
Best Local Similarity 60.0%; Pred. No. 5.2e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKIS 6

Db 2 TMKLS 6

## RESULT 9

US-10-162-497-78  
; Sequence 78, Application US/10162497  
; Publication No. US20030158398A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, H.  
; APPLICANT: Freimer, N.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CHROMOSOME-16P RELATED DISORDERS  
; FILE REFERENCE: 7853-138  
; CURRENT APPLICATION NUMBER: US/10/162,497  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US/09/657,474  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 09/268,392  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/106,056  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: 60/088,312  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/078,044  
; PRIOR FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 78  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-162-497-78

Query Match 54.5%; Score 18; DB 12; Length 7;  
Best Local Similarity 50.0%; Pred. No. 5.2e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKIS 6

Db 2 YTMKYS 7

## RESULT 10

US-10-105-930-39  
; Sequence 39, Application US/10105930

```
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, Ko. US20030009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: JP 11-273359
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-39

Query Match      51.5%; Score 17; DB 15; Length 6;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKI 5
   :|||:
Db 1 YTSQI 5

RESULT 11:
US-10-043-539-30
; Sequence 30, Application US/10043539
; Publication No. US20030114650A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Ambrose
; APPLICANT: Manna, Adar
; APPLICANT: Zhang, Gorgyi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
; TITLE OF INVENTION: BACTERIA
; FILE REFERENCE: DC-0199
; CURRENT APPLICATION NUMBER: US/10/043,539
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,233
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,607
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/289,601
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539-30

Query Match      51.5%; Score 17; DB 15; Length 6;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKISR 7
   :|||:
Db 2 IKITR 6

RESULT 12
US-09-996-288-135
; Sequence 135, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James

; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylax
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-135

Query Match      51.5%; Score 17; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKIS 6
   :|||:
Db 2 TLKLA 6

RESULT 13
US-09-996-265-135
; Sequence 135, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylax
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-135

Query Match      51.5%; Score 17; DB 11; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKIS 6
   :|||:
Db 2 TLKLA 6

RESULT 14
US-10-044-034-13
; Sequence 13, Application US/10044034
; Publication No. US20020169264A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.
; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FBRC:006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 13  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptides  
JS-10-044-034-13

Query Match 51.5%; Score 17; DB 14; Length 7;  
Best Local Similarity 60.0%; Pred. No. 5.2e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

>Y 2 TLKIS 6  
|||  
>b 1 TLKLA 5

RESULT 15  
S-09-727-963A-88  
Sequence 88, Application JS/09727963A  
Patent No. US20020155106A1  
GENERAL INFORMATION:  
APPLICANT: V.I. Technologies, Inc.  
APPLICANT: Hammod, David J.  
TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
FILE REFERENCE: 18242-505  
CURRENT APPLICATION NUMBER: US/09/727,963A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
PRIOR FILING DATE: 1999-12-02  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 88  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand  
NAME/KEY: VARIANT  
LOCATION: (1)  
OTHER INFORMATION: wherein Xaa is D-phenylalanine  
JS-09-727-963A-88

Query Match 48.5%; Score 16; DB 10; Length 6;  
Best Local Similarity 75.0%; Pred. No. 5.2e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

>Y 1 FTLK 4  
|||  
>b 3 FTFK 6

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ob time : 34.6667 secs

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protein - protein search, using sw model

run on: October 4, 2003, 12:42:47 ; Search time 17 Seconds  
(without alignments)  
17.422 Million cell updates/sec

title: US-09-712-819C-6  
effect score: 33  
sequence: 1 FTLKISR 7

scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

searched: 328717 seqs, 42310358 residues

total number of hits satisfying chosen parameters: 43738

minimum DB seq length: 0  
maximum DB seq length: 7

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : Issued Patents AA.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	7	1	US-08-222-619-8
2	20	60.6	7	5	PCT-US95-04075-8
3	19	57.6	6	6	5252328
4	18	54.5	7	2	US-08-346-333-24
5	18	54.5	7	4	US-09-268-992-78
6	18	54.5	7	4	US-09-657-474-78
7	18	54.5	7	5	PCT-US91-07506-24
8	17	51.5	7	2	US-09-174-060-17
9	17	51.5	7	3	US-08-654-623-69
10	17	51.5	7	3	US-08-338-382-17
11	16	48.5	5	3	US-08-591-632-23
12	16	48.5	5	4	US-09-611-451-23
13	16	48.5	6	2	US-07-717-331F-5
14	16	48.5	6	4	US-08-757-425B-44
15	16	48.5	7	2	US-07-634-641-12
16	16	48.5	7	2	US-08-136-743B-55
17	16	48.5	7	3	US-09-040-216-28
18	16	48.5	7	3	US-09-173-941-72
19	16	48.5	7	4	US-09-423-469A-6
20	16	48.5	7	4	US-09-756-223A-26
21	15	45.5	4	2	US-08-305-871A-17
22	15	45.5	4	4	US-08-788-822A-1
23	15	45.5	4	4	US-08-134-231C-36
24	15	45.5	5	1	US-08-136-743B-63
25	15	45.5	5	3	US-09-040-216-55
26	15	45.5	5	3	US-08-591-632-17
27	15	45.5	5	3	US-08-591-632-26

Sequence 17, Appl  
Sequence 26, Appl  
Sequence 62, Appl  
Sequence 6, Appl  
Sequence 4, Appl  
Sequence 21, Appl  
Sequence 41, Appl  
Sequence 6, Appl  
Sequence 41, Appl  
Sequence 41, Appl  
Sequence 219, App  
Sequence 219, App  
Sequence 54, Appl  
Sequence 6, Appl  
Sequence 41, Appl  
Sequence 219, App  
Sequence 650, App

ALIGNMENTS

RESULT 1  
US-08-222-619-8  
; Sequence 8, Application US/05222619  
; Patent No. 5652352  
; GENERAL INFORMATION:  
; APPLICANT: Lichenstein, Henri  
; APPLICANT: Lyons, David  
; APPLICANT: Wurfel, Mark  
; APPLICANT: Wright, Samuel  
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like  
; TITLE OF INVENTION: Protein  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Center, Patent Operations/RRC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,619  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-222-619-8

Query Match 60.6%; Score 20; DB 1; Length 7;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0;

Qy 1 FTLKISR 7  
|||  
Db 1 FTFEYSR 7

RESULT 2  
PCT-US95-04075-8  
; Sequence 8, Application PC/TUS9504075  
; GENERAL INFORMATION:



APPLICANT: AMGEN INC.  
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Center, Patent Operations/FAC  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: U.S.  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04075  
FILING DATE:

CLASSIFICATION:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US95-04075-8

Query Match 60.6% Score 20; DB 5; Length 7;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY : FTLKISR 7  
|| : ||  
Db 1 PTFEYSR 7

RESULT 3  
252328-8  
Patent No. 5252328  
APPLICANT: FAJLOS,DARYL;VISHOOT,MIMI;BROCKS,EMILY  
TITLE OF INVENTION: MYOPLASMA HYOPNEUMONIAE ANTIGEN AND USES  
THEREFORE

NUMBER OF SEQUENCES: 15  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/335,726  
FILING DATE: 07-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 30,130  
FILING DATE: 26-MAR-1987

SEQ ID NO:8:  
LENGTH: 6  
252328-8

Query Match 57.6% Score 19; DB 6; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKI 5  
||| : |||  
Db 2 FVLKI 6

RESULT 4  
US-08-346-333-24  
Sequence 24, Application: US/05346333  
Patent No. 5677153  
GENERAL INFORMATION:  
APPLICANT: Botstein, David  
APPLICANT: Palzkill, Timothy  
TITLE OF INVENTION: Methods for modifying DNA and for  
TITLE OF INVENTION: detecting effects of such modification on interaction of

TITLE OF INVENTION: encoded modified polypeptides with target substrates.  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard F. Trecartin  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,333  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/039,501  
FILING DATE:  
APPLICATION NUMBER: US 07/602,159  
FILING DATE: 22-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,601  
REFERENCE/DOCKET NUMBER: A-53469/RFT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-333-24

Query Match 54.5% Score 18; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5  
||| : |||  
Db 2 TLKI 5

RESULT 5  
US-09-268-992-78  
Sequence 78, Application US/99268992  
Patent No. 6342351  
GENERAL INFORMATION:  
APPLICANT: Chen, H.  
APPLICANT: Preimer, N.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS  
FILE REFERENCE: 7853-138  
CURRENT APPLICATION NUMBER: US/09/268,992  
CURRENT FILING DATE: 1999-03-16  
EARLIER APPLICATION NUMBER: 09/236,134  
EARLIER FILING DATE: 1999-01-22  
EARLIER APPLICATION NUMBER: 60/106,056  
EARLIER FILING DATE: 1998-10-28  
EARLIER APPLICATION NUMBER: 60/089,312  
EARLIER FILING DATE: 1998-06-05  
EARLIER APPLICATION NUMBER: 60/079,044  
EARLIER FILING DATE: 1998-03-16  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 78  
LENGTH: 7  
TYPE: PRT

ORGANISM: Homo sapiens  
S-09-268-992-78

Query Match 54.5%; Score 18; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 FTLKIS 6  
b 2 YTMKYS 7

RESULT 6  
S-09-657-474-78  
Sequence 78, Application US/09657474  
Patent No. 6399762  
GENERAL INFORMATION:  
APPLICANT: Chen, H.  
APPLICANT: Freimer, N.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS  
FILE REFERENCE: 7953-136  
CURRENT APPLICATION NUMBER: US/09/657,474  
CURRENT FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: 09/268,992  
PRIOR FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 09/236,134  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/106,356  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/088,312  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/078,044  
PRIOR FILING DATE: 1998-03-16  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 78  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
S-09-657-474-78

Query Match 54.5%; Score 18; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 FTLKIS 6  
b 2 YTMKYS 7

RESULT 7  
CT-US91-07506-24  
Sequence 24, Application PC/TUS9107506  
GENERAL INFORMATION:  
APPLICANT: Botstein, David  
APPLICANT: Palakill, Timothy  
TITLE OF INVENTION: Methods for modifying DNA and for  
TITLE OF INVENTION: detecting effects of such modification on interaction of  
TITLE OF INVENTION: encoded modified polypeptides with target substrates.  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard F. Trecartin  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DCS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07506  
FILING DATE: 19911021  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: FP-53469-PC/RFT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US91-07506-24

Query Match 54.5%; Score 18; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5  
b 2 TLKI 5

RESULT 8  
US-09-174-060-17  
Sequence 17, Application US/09174060  
Patent No. 5989554  
GENERAL INFORMATION:  
APPLICANT: Knuth, Mark W  
APPLICANT: Haak-Frendscho, Mary  
APPLICANT: Shultz, John W  
APPLICANT: Lesley, Scott A  
APPLICANT: Villars, Catherine E  
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE  
TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR  
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ross & Stevens, S.C.  
STREET: 1 South Pinckney St.  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/174,060  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/338,382  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-257-5353  
TELEFAX: 608-257-9175  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein

JS-09-174-060-17

Query Match 51.5% Score 17; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4  
: : :  
Cb 1 YTLK 4

RESULT 9

US-08-654-623-69  
Sequence 69, Application US/08654623  
Patent No. 6010884  
GENERAL INFORMATION:  
APPLICANT: Griffiths, Andrew D  
APPLICANT: Holliger, Kaspar-Philipp  
APPLICANT: Nissim, Ahuva  
APPLICANT: Fisch, Igor  
APPLICANT: Winter, Gregory F  
TITLE OF INVENTION: Recombinant Binding Proteins and Peptides  
NUMBER OF SEQUENCES: 7;  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO);  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/654,623  
FILING DATE: 29-MAY-1996

CLASSIFICATION: 435  
CLASSIFICATION: (C12N 1/21, C12R 1:19)  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9225453.1  
FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9300816.7  
FILING DATE: 16-JAN-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93303614.7  
FILING DATE: 10-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9319969.3  
FILING DATE: 22-SEP-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/02492  
FILING DATE: 03-DEC-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9412147.2  
FILING DATE: 17-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/02462  
FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/448,418  
FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33259

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-654-623-69

Query Match 51.5% Score 17; DB 3; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKIS 6  
: : : :  
Cb 1 SLKVS 5

RESULT 10

US-08-338-382-17  
Sequence 17, Application US/08338382  
Patent No. 6059230  
GENERAL INFORMATION:

APPLICANT: Knuth, Mark W  
APPLICANT: Haak-Frendscho, Mary  
APPLICANT: Shultz, John W  
APPLICANT: Lesley, Scott A  
APPLICANT: Villars, Catherine E  
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE  
TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR  
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ross & Stevens, S.C.  
STREET: 1 South Pinckney St.  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,382  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S

REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 34506.024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-257-5353  
TELEFAX: 608-257-9175

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-338-382-17  
Query Match 51.5% Score 17; DB 3; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4  
: : :  
Cb 1 YTLK 4

RESULT 11

S-08-591-632-23  
Sequence 23, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 2  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
-08-591-632-23

Query Match 48.5%; Score 16; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 FTLK 4  
|||  
2 FTLQ 5

RESULT 12  
-09-611-451-23  
Sequence 23, Application US/09611451  
Patent No. 6395275  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/611,451  
FILING DATE: 06-Jul-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/591,632  
FILING DATE: 2001-10-29  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-611-451-23

Query Match 48.5%; Score 16; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4  
|||  
Db 2 FTLQ 5

RESULT 13  
US-07-717-331F-5  
Sequence 5, Application US/C7717331F  
Patent No. 5484905  
GENERAL INFORMATION:  
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua  
APPLICANT: Stein  
TITLE OF INVENTION: A Receptor Protein Kinase Gene  
TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/717,331F  
FILING DATE: June 19th 1991  
CLASSIFICATION: 80C  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yawwak  
REGISTRATION NUMBER: 26,824  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
S-07-717-331F-5

Query Match 48.5%; Score 16; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 3 LKIS 6  
|||  
b 2 LKVS 5

RESULT 14  
S-08-757-425B-44  
Sequence 44, Application US/08/757425B  
Patent No. 6500660  
GENERAL INFORMATION:  
APPLICANT: Fastrez, Jacques  
TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity  
FILE REFERENCE: 100390-09640  
CURRENT APPLICATION NUMBER: US/08/757,425B  
CURRENT FILING DATE: 1996-11-27  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 44  
LENGTH: 6  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Mimotope  
S-08-757-425B-44

Query Match 48.5%; Score 16; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 2 TLKIS 6  
|||  
b 2 TAKVS 6

RESULT 15  
S-07-634-641-12  
Sequence 12, Application US/07634641  
Patent No. 5386011  
GENERAL INFORMATION:  
APPLICANT: Wiedeman, Paul E.  
APPLICANT: Kawai, Megumi  
APPLICANT: Luly, Jay R.  
APPLICANT: Cr, Yat-Sur  
APPLICANT: Wagner, Rolf  
TITLE OF INVENTION: Hexa- and Heptapeptide Anaphylatoxin  
TITLE OF INVENTION: Receptor Ligands  
NUMBER OF SEQUENCES: 2;  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: One Abbott Park Road  
CITY: No. 5386011th Chicago  
STATE: IL

COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,641  
FILING DATE: 19901227  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Janssen, Jerry F.  
REGISTRATION NUMBER: 29,175  
REFERENCE/DOCKET NUMBER: 4934.JS.O1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 937-4558  
TELEFAX: (708) 937-9556  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
JS-07-634-641-12  
Query Match 48.5%; Score 16; DB 1; Length 7;  
Best Local Similarity 28.6%; Pred. No. 2.5e+05;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
CY 1 FTLKISR 7  
|::|  
Cb 1 FMRLGR 7  
Search completed: October 4, 2003, 12:50:25  
Job time : 18 secs